

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 27.6718 Seconds

(without alignments)
834.495 Million cell updates/sec

Title: US-10-029-926d-235

Perfect score: 1266

Sequence: 1 MAEVLVESGGVVRPGSL.....RDSGNHVVGSGTFLTVIG 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	46.3	268	2 A56446	Ig heavy chain V r
2	586	44.9	109	2 S19663	Ig lambda chain V
3	562	44.4	108	2 S47184	Ig lambda chain -
4	561.5	44.4	249	2 S41374	single chain Fv an
5	551.5	43.6	110	2 S36272	Ig lambda chain V
6	546	43.1	127	2 S70444	Ig lambda chain pr
7	541	42.7	108	2 S38498	Ig lambda chain -
8	539	42.6	109	2 S38496	Ig lambda chain -
9	530	41.9	233	2 S25748	Ig lambda chain -
10	527	41.6	108	1 L3HUSH	Ig lambda chain V -
11	522.5	41.3	233	2 JCS322	p53 specific shngl
12	518.5	41.0	110	2 S19672	Ig lambda chain V
13	517.5	40.9	146	2 S02083	Ig lambda chain V -
14	513	40.5	98	2 S26928	Ig heavy chain V r
15	510.5	40.3	128	2 S31595	Ig heavy chain V r
16	503	39.7	96	2 S36060	Ig lambda chain -
17	503	39.7	115	2 S13726	Ig lambda chain V
18	503	39.7	121	2 S31118	Ig heavy chain - h
19	502	39.7	123	2 S30532	Ig heavy chain V r
20	502	39.7	233	2 S25741	Ig lambda chain -
21	495.5	39.1	121	2 S31104	Ig heavy chain (su
22	495.5	39.1	112	2 PH1654	Ig heavy chain V r
23	491	38.8	120	2 S36273	Ig heavy chain V r
24	488	38.5	138	2 S31599	Ig heavy chain V r
25	487	38.5	138	2 S31566	Ig heavy chain V r
26	485.5	38.3	120	2 S44111	Ig heavy chain V-D
27	485.5	38.3	145	2 S11239	Ig heavy chain V r
28	485	38.3	119	2 S31108	Ig heavy chain - h
29	485	38.3	160	2 S05271	Ig heavy chain pre

30	484.5	38.3	120	2 S48798	Ig heavy chain V r
31	482	38.1	119	2 S31107	Ig heavy chain - h
32	480	37.9	121	2 S55673	Ig heavy chain - h
33	480	37.9	123	2 S31114	Ig heavy chain - h
34	478	37.8	119	2 D36005	Ig heavy chain V r
35	477	37.7	140	2 S31686	Ig heavy chain V r
36	476	37.6	119	2 C36005	Ig heavy chain V r
37	475	37.5	139	2 S37781	Ig variable region
38	473.5	37.4	124	2 S20782	Ig heavy chain V r
39	473.5	37.4	128	2 S26790	Ig heavy chain V r
40	473.5	37.4	140	2 S70442	Ig heavy chain pre
41	473.5	37.4	151	2 A60943	Ig heavy chain pre
42	473	37.4	127	2 S38489	Ig heavy chain - h
43	473	37.4	135	2 S31598	Ig heavy chain V r
44	472	37.3	98	2 S25927	Ig heavy chain V r
45	472	37.3	143	2 S23624	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #ext_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity dioxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TRAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 46.3%; Score 586; DB 2; Length 268;

Best Local Similarity 50.6%; Pred. No. 1.1e-33;

Matches 123; Conservative 34; Mismatches 78; Indels 8; Gaps 5;

QY	1	MAEVLVESGGVVRPGSLRSCASGFTPDYGMWVRQAPKGLWVSGINMNGST 60	
DB	1	MAOVKLQESGAEIVKFGASVLCSTTSGRNFKDTYHAWKORPEQGLWIGRIAPANGIT 60	
QY	61	GYADSVKGRFTISRDNKNSLYLQWNSLRAPDPAVYCAR---MRAPVIMGGCTLYTVSR 117	
DB	61	KYDPKFGKATIAADTSNTAVYQLSLTSEDTAVYVCASYLTRYENTWGGCTTVTS 120	
QY	118	GGGSGGGSGSGSGSS-ELTQDPAY-SVALGQTVRTCCGDSLRSTYASWYQQKPGQAPV 175	
DB	121	GGGSGGGSGSGSGSGSDIELTQSPAIMSASLGEKVTMSCPASSSVN-FIYVQQKSDASPK 179	
QY	176	LVYVGNKRPSCGIPDFSSSGNTASTLTITGAQADEADYVYCNSSDGNHVPFGGTR 235	
DB	180	LWVYTSHPGVPARFSSGSGNSYSLTISMEGSDAATVYCCQFTSS--PTFSGTK 237	
QY	236	LTV 238	
DB	238	LEI 240	
RESULT 2			
S19663 Ig lambda chain V region (clone alpha-B5A3) - human			
C/Species: Homo sapiens (man)			
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #ext_change 20-Jun-2000			
C/Accession: S19663			
R/Mark, J.D.; Hoogenboom, H.R.; Bonnet, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991			
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage			
A/Reference number: S19663; PMID:92085276; PMID:1748994			

A/Accession: S19663
A/Molecule type: mRNA
A/Residues: 1-109 <MAR>
A/Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA4821.1; PID:g1340166
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 568; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 7.8e-33;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGOTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 191
Db 1 SSELTDPAVVALGOTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEADDDYCNRRDSSGNHVFPGGKTTLVLG 240
Db 61 FSGSSSGNTASLTITGAQAEADDDYCNRRDSSGNHVFPGGKTTLVLG 109

RESULT 3

S47184
Ig Lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S47184
R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

Submitted to the EMBL Data Library, June 1994
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A/Reference number: S47181
A/Accession: S47184

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <MCI>
A/Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 44.4%; Score 562; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2e-32;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGOTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 191
Db 1 SSELTDPAVVALGOTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEADDDYCNRRDSSGNHVFPGGKTTLVL 239
Db 61 FSGSSSGNTASLTITGAQAEADDDYCNRRDSSGNHVFPGGKTTLVL 108

RESULT 4

S41374
Single chain Fv antibody - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374
R/Atsessenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
Submitted to the EMBL Data Library, January 1994
A/Description: Construction and functional characterization of a single chain Fv antibody
A/Reference number: S41374
A/Accession: S41374
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <ART>
A/Cross-references: EMBL:Z29480

Query Match 44.4%; Score 561.5; DB 2; Length 249;
Best Local Similarity 48.6%; Pred. No. 5.2e-32;
Matches 121; Conservative 36; Mismatches 71; Indels 21; Gaps 6;

QY 3 EVQLVESGGGVVPPGSLRLSCAASGFTPDYGMKSWROAPGKGLMEWSINMGSTGY 62
Db 1 OVLOQSGAEIVRPGASVLTCTASGFNPKDYLHVVKORPKGLEIMIRIAPASGNVXX 60

QY 63 ASVYKRFITISDNMANSIYTIOMNSLRADPTVYVCAR----MRAPVIGGGTLVYVSRG 118
Db 61 VRFPODKATITADTSSNTAVYLLSLTSDTAVYCARDDTLVTSIGVYGGQSTVTVSSR 120

QY 119 GGGSGGGSGGGSS-ELTQD--PAVVALGOTVRITTCQ-----GDSLRSYASWYQ 167
Db 121 GGGSGGGSGGGSDLELTQSPSVVIRPGESVISCRSKSLVSDGS----YLFWFL 176

QY 168 QKPGQAPVLVIYGNRPSGIPDRFSGSSGNTASLTITGAQAEADDDYCNRRDSSGNH 227
Db 177 QKPGQAPVLVIYGNRPSGIPDRFSGSSGNTASLTITGAQAEADDDYCNRRDSSGNH 234

QY 228 VVFGGKTTL 236
Db 235 LTFGAGTKL 243

RESULT 5

S36272
Ig Lambda chain V region (clone alpha-THY-29) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36272
R/Giffiths, A.D.; Malmyvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; NID:93178448; PMID:7679990
A/Accession: S36272
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1110 <GRI>
A/Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g933912
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.6%; Score 551.5; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.1e-31;
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 132 SSELTDPAVVALGOTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 191
Db 1 SSELTDPAVVALGOTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEADDDYCNRRDSSGNHVFPGGKTTLVLG 240
Db 61 FSGSSSGNTASLTITGAQAEADDDYCNRRDSSGNHVFPGGKTTLVLG 110

RESULT 6

S70444
Ig Lambda chain precursor V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: S70444; S70426
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IgM kappa/Lambda EBV human B cell clone: an early step of differentiation of B
A/Reference number: S70442; NID:93024508; PMID:1383695
A/Accession: S70444
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-127 <CUI>
A/Cross-references: UNIPROT:Q9NSD6
A/Experimental source: clone E29.1
R/Tonnelle, C.
Submitted to the EMBL Data Library, May 1990
A/Reference number: S70426
A/Accession: S70426

Query Match 44.4%; Score 561.5; DB 2; Length 249;
Best Local Similarity 48.6%; Pred. No. 5.2e-32;
Matches 121; Conservative 36; Mismatches 71; Indels 21; Gaps 6;

A:Molecule type: mRNA
 A:Residues: 1-90 <TON>
 A:Cross-references: EMBL:X53070
 A:Experimental source: cell line E29.1, clone VL 29-1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
 F:14-108/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 546; DB 2; Length 127;
 Best Local Similarity 97.2%; Pred. No. 3e-31;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 191
 |||||
 DB 20 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 79

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 239
 |||||
 DB 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 127

RESULT 7

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S38498
 R:Marx, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
 submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from a F

A:Reference number: S38488
 A:Accession: S38498
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-108 <MAR>
 A:Cross-references: EMBL:Z23035; NID:g414043; PIDN:CAA80570.1; PID:g414044
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 42.7%; Score 541; DB 2; Length 108;
 Best Local Similarity 97.2%; Pred. No. 5.7e-31;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 133 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 192
 |||||
 DB 1 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60

QY 193 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 240
 |||||
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 108

RESULT 8

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S38496
 R:Marx, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
 submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from a F

A:Reference number: S38488
 A:Accession: S38496
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-109 <MAR>
 A:Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 42.6%; Score 539; DB 2; Length 109;

Best Local Similarity 93.6%; Pred. No. 7.9e-31;
 Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 191
 |||||
 DB 1 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 240
 |||||
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 109

RESULT 9

Ig lambda chain - human

C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S25748
 R:Combracio, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin la

A:Reference number: S16439; NID:91257162; PMID:1904362
 A:Accession: S25748
 A:Status: preliminary; translation not shown

A:Molecule type: mRNA
 A:Residues: 1-233 <COM>
 A:Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 530; DB 2; Length 233;

Best Local Similarity 91.7%; Pred. No. 7.3e-30;
 Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 191
 |||||
 DB 20 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 79

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 240
 |||||
 DB 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 128

RESULT 10

Ig lambda chain V-III region (Sh) - human

C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A01980
 R:Titani, K.; Wikler, M.; Shindou, T.; Putnam, F.W.
 J. Biol. Chem. 245, 2171-2176, 1970

A:Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete

A:Reference number: A92057; NID:70166723; PMID:4909564
 A:Accession: A01980
 A:Molecule type: protein
 A:Residues: 1-108 <TIT>

A:Cross-references: UNIPROT:P01714
 A>Note: the sequence of the C region is also given

C:Genetics:

A:Gene: GDB:IGLV6
 A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k

C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>
 F:21-86/Disulfide bonds: #status experimental

Query Match 41.6%; Score 527; DB 1; Length 108;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 123.991 Seconds

(without alignments)
991.192 Million cell updates/sec

Title: US-10-029-926d-235

Perfect score: 1266
Sequence: 1 MAEVLVESGGVVRPGSL.....RDSGNHVVRGGSTKLTVLG 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	59.9	240	2	065ZC9
2	715	56.5	255	2	06KX05
3	695.5	54.9	248	2	065Z07
4	691.5	54.6	258	2	09QYF0
5	636	50.2	244	2	065ZC8
6	600	47.4	241	2	0921A6
7	578	45.7	243	2	07TQW2
8	552	43.6	107	2	09NSD6
9	550.5	43.5	112	2	09HCT1
10	348	43.3	487	2	065ZL2
11	530	41.9	233	2	06GMM4
12	527	41.6	108	1	LV3A_HUMAN
13	512	40.4	472	2	06N0B9
14	510	40.3	499	2	08NSK4
15	507.5	40.1	218	2	0925S1
16	504	39.8	173	2	08WJ38
17	483	38.2	121	2	09UL71
18	476	37.6	470	2	06PUJ4
19	476	37.6	478	2	06PI81
20	476	37.6	606	2	06GMV2
21	473	37.4	613	2	08WUK1
22	472.5	37.3	557	2	096BB9
23	472	37.3	464	2	06MZ06
24	470	37.1	113	2	09UL90
25	465.5	36.8	473	2	06MZV7
26	464	36.7	493	2	06GMX2
27	461.5	36.5	118	2	09UL91
28	456.5	36.1	475	2	06MZ06
29	455	35.9	466	2	06IN78
30	452.5	35.7	479	2	06MZV6
31	446.5	35.3	116	1	HV3T_HUMAN

32	444.5	35.1	122	1	HV3G_HUMAN
33	444	35.1	116	2	09UL93
34	444	35.1	473	2	091Z05
35	442.5	35.0	465	2	06PC4
36	442	34.9	117	1	HV3C_HUMAN
37	440.5	34.8	494	2	096K68
38	438.5	34.6	483	2	06MZX9
39	438.5	34.6	494	2	06ZW64
40	438.5	34.6	544	2	06PJ95
41	438	34.6	479	2	091WP5
42	436.5	34.5	118	2	09UL72
43	436.5	34.5	475	2	06GMV7
44	434	34.3	233	2	08TBC9
45	434	34.3	480	2	06N094

ALIGNMENTS

RESULT 1

ID	Q65ZC9	PRELIMINARY;	PRT;	240 AA.
AC	Q65ZC9;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Single-chain Fv (Fragment).			
GN	Name=ScFv;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C1q/7;			
RX	MEDLINE=97362799; PubMed=9219263;			
RA	Kontermann R.B., Wing M.G., Winter G.;			
RT	"Complement recruitment using bispecific diabodies."			
RL	Nat. Biotechnol. 15:629-631(1997).			
DR	EMBL; Y13056; CAJ73499.1; -.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig_Like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; Ig; 2.			
DR	SMART; SM00406; IgV; 2.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
FT	NON_TER 1			
FT	NON_TER 240			
SQ	SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;			

Query Match 59.9%; Score 758; DB 2; Length 240;
Best local similarity 62.9%; Pred. No. 5,7e-48;
Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;

QY	3	EVOLVESGGVVRPGSLRISCAASGFTPDYGSWVRQAPGKLEVAISGNNKGGSTGY 62
DB	1	QVQVLVDSGGGLVDPGSLRISCAASGFTFSYGNHWRQAPGKLEVAIAISTGSKYY 60
QY	63	ADVVKGRFTTISRNNAKSLYLQNNSLRAEDTAVVYCARMAPVY--NGOGTLVTVSRGGG 120
DB	61	ADVVKGRFTTISRNNAKSLYLQNNSLRAEDTAVVYCARMDGSLDIPGKKTIVTVSSGGG 120
QY	121	GSGGGGSGGGGSS-ELTQDPA-VSVALGQTVRTTCGDSLRSTYASVYQKPGQAPLVY 178
DB	121	GSGGGGSGGGGSDIQWQSPSTISASIGDVTTCRASEGIYVWLAVYQKPGAPVLLI 180
QY	179	YGNKNRPSGIPDRFSSSGSSNTASLTITGAQAEADADYCNRSDDSGNHVVRGGSTLTIV 238
DB	181	YKASLSLRAPSRPSGSGSTDTLTITSSIQDPDPFATYVC--QQVSNYPLPFGGTLLEI 238

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06KB05
ID 06KB05 PRELIMINARY; PRT; 255 AA.
AC 06KB05;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE SCFV B8E5 protein (Fragment).
GN Name=scfV B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.,
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL, AJ746180; CAG34081.1; -.
DR HSSP, P01837; IKCR.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART, SM00409; IG; 2.
DR SMART, SM00406; IGV; 2.
DR PROSITE, PSS0835; IG LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD3835DF713B CRC64;

Query Match 56.5%; Score 715; DB 2; Length 255;
Best Local Similarity 58.8%; Pred. No. 8.8e-45;
Matches 147; Conservative 33; Mismatches 54; Indels 16; Gaps 6;

QY 3 EVOLVSSGGGVNRPGLSLSCAAGFTPDDYGMVNRQAPGKLEWVSGINMGSTGY 62
DB 1 QVQLQOSGGDVLVPRGSLKVCASGFTFSYSMSWRQTPDRKLEVAITITSGSYTY 60
QY 63 ADSVKGRFTISRDNANKSLYLQKNSLRADPTAVYYCARM-----RAPVWGQGLTVTVS 116
DB 61 PDSVKGRFTISRDNANKSLYLQKNSLRKSEDTAVYYCARHINRYDAGFDYWGQGLTVTVS 120
QY 117 RGGGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCQ-GDSL-----RSYYASWYQQ 168
DB 121 SGGGGGGGGGGGGGSDIVVAQSPSSLSVSGAGEKIVMSCKSQSLNSRNQKYLAWYQQ 180
QY 169 KPGQAPVLVIYKGNRPSSGIPDRFSGSSSGNTASLTITGAQADEADYICNSRDSGNHY 228
DB 181 KPQSPPLLIYGASTRSGVDPDRFTSGSGGTDFTLTISVQABDLAVYICQNDHS--YPL 238
QY 229 VFGGGLTV 238
DB 239 TRGAGTKLEI 248

RESULT 3
06SZ07 PRELIMINARY; PRT; 248 AA.
AC 06SZ07;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DE B3(FV)-PE40 (Fragment).
GN Name=B3(FV)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92020904; Pubmed=1924323;
RA Brinkmann U., Pal L.H., Fitzgerald D.J., Williamson M., Paetan I.,
RA "B3(FV)-PE38KDEL", a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice."

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RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL, S57990; AAB19971.2; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam, PF00047; IG; 2.
DR SMART, SM00409; IG; 2.
DR SMART, SM00406; IGV; 2.
DR PROSITE, PSS0835; IG LIKE; 2.
FT NON_TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 54.9%; Score 695.5; DB 2; Length 248;
Best Local Similarity 57.8%; Pred. No. 2.3e-43;
Matches 144; Conservative 32; Mismatches 56; Indels 17; Gaps 6;

QY 3 EVOLVSSGGGVNRPGLSLSCAAGFTPDDYGMVNRQAPGKLEWVSGINMGSTGY 62
DB 2 DVKLVSGGGLVQPGSLKSLCATSGFTSDYMWVWRQTPKRLKLEVAITISNDSSAAV 61
QY 63 ADSVKGRFTISRDNANKSLYLQKNSLRADPTAVYYCARM-----PVIWGQGLTVTVSRG 118
DB 62 SDTVKGRFTISRDNANKSLYLQKNSLRKSEDTAVYYCARGLANGAWFAVWGQGLTVTVSSG 121
QY 119 GGGGGGGGGGGSSSEL-TQDP-AVSVALGQTVRITCQDST-----RSYYASWYQQKPG 171
DB 122 GGGGGGGGGGGSDVLTMTQSLPLVSLGDQASISCRSSQITVHSGNTYLEWYLQKPG 181
QY 172 QAPVLVIYKGNRPSSGIPDRFSGSSSGNTASLTITGAQADEADYICNSRDSGNHY--V 229
DB 182 QSPKLIYKVNINFPVSGVDPDRFSGSGGTDFTLTISVQABDLGVYC-----FGSHVPT 237
QY 230 FGGGGLTV 238
DB 238 FSGTKLEI 246

RESULT 4
09GYF0 PRELIMINARY; PRT; 298 AA.
AC 09GYF0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE CN 8 single chain antibody.
GN Name=CN 8 scfv;
OS Synthetic construct.
OC Other sequences; artificial sequences.
OX NCBI_TaxID=32630;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20183931; Pubmed=10706631; DOI=10.1073/pnas.050582197;
RA Shinonara N., Demura T., Fukuda H.,
RA "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL, AB036341; BA086633.1; -.
DR PIR, A33933; A33933.
DR PIR, S19112; S19112.
DR HSSP, P01820; IAYO.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART, SM00406; IGV; 2.
DR PROSITE, PSS0835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 54.6%; Score 691.5; DB 2; Length 298;
Best Local Similarity 56.0%; Pred. No. 5.5e-43;
Matches 139; Conservative 28; Mismatches 64; Indels 17; Gaps 5;

QY 1 MAEVLVSSGGGVNRPGLSLSCAAGFTPDDYGMVNRQAPGKLEWVSGINMGSTGY 60

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Db      38 MAQVKLQSGGGLVKRPGSLKSLSCAASGDSFRRYMWVWRQAPKGLWIGELINPDSTI 97
Qy      61 GYADSVKGRFTISRDNKNSLYLQNMSLRAEDTAVVYCARMR---APVIMGGTTLTVSR 117
Db      98 NTPSLKDKFIIISRDNKNSLYLQNMSEDTALTYCAASYYGSHANWGQGTIVVSS 157
Qy      118 GGGGSGGGSGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYYASWYQOKPGQAPV 175
Db      158 GGGGSGGGSGGGGSDIELQSPASISASVGETVITTCRASGNIHNYLAWYQOKPGKSPQ 217
Qy      176 LVYIGKNNRPSGIPDRFSGSSGNTASLTGQAQAEADYCNRSDDSGNH---VVF 230
Db      218 LVLVYNAKTLADYGPSPRFSGSGSTGYSLKINSIQPEDFGSYC-----QHFMTTPYTF 270
Qy      231 GGGTTLTV 238
Db      271 GGGTKLEI 278

RESULT 5
ID 065ZC8 PRELIMINARY; PRT; 244 AA.
AC 065ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scfv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=97362799; PubMed=9219263;
Konfermann R.E., Wing M.G., Wintex G.;
"Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17686338F2BF CRC64;

Query Match 50.2%; Score 636; DB 2; Length 244;
Best Local Similarity 50.8%; Pred. No. 5.3e-39;
Matches 124; Conservative 46; Mismatches 64; Indels 10; Gaps 4;

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RESULT 6
ID 0921A6 PRELIMINARY; PRT; 241 AA.
AC 0921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=98170165; PubMed=9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Ra Y.I., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; IBMV.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 47.4%; Score 600; DB 2; Length 241;
Best Local Similarity 51.9%; Pred. No. 2.3e-36;
Matches 126; Conservative 34; Mismatches 67; Indels 16; Gaps 6;

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Qy      3 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMVWRQAPGKLEWISGNNGSTGY 62
Db      1 QVQLVSGAEVKKPGQSLVKSCAKASGTTTSDHMHWRQAPGQGLEWGMGIDPNNEDTFR 60
Qy      63 ADSVKGRFTISRDNKNSLYLQNMSLRAEDTAVVYCAR---MRAPVIMGGTTLTVS 116
Db      61 AGRFGQRTVMTTRTSTSAAMAEVSRISRDDTAVYYCARBETGSAIYGMQVWGQGLTVVS 120
Qy      117 RGGGSGGGSGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYYASWYQOKPGQAP 174
Db      121 SGGGSGGGSGGGGSDIQWTQSPSTLSASIGRVTITCASBGITHTWLAWYQOKPGKAP 180
Qy      175 VLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYCNRSDDSGNNVVFQGGT 234
Db      181 KPLIYKASLSASGAPRFSGSGSTPTLTISLQPDPAFYIC--QQYISNYLITRGGT 238
Qy      235 KLTIV 238
Db      239 KLEI 242

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RESULT 7
ID 07TQM2 PRELIMINARY; PRT; 243 AA.
AC 07TQM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE scfv 6H8 protein (Fragment).
GN Name=scfv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

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RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/C;
 RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
 RA Peter U.C.; Eftekhari P.; Billiald P.; Wallukac G.; Hoebeke J.;
 RT "acv single chain antibody variable fragment as inverse agonist for
 the beta-2 adrenergic receptor";
 RL J. Biol. Chem. 278:36740-36747(2003).
 DR EMBL: AJ574851; CAE00495.1; -.
 DR HSSP: P01751; 1A6W.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 2.
 DR PROSITE: PS50835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 243 AA; 25976 MW; BEFF642DDCF4F76 CRC64;

Query Match 45.7%; Score 578; DB 2; Length 243;
 Best Local Similarity 49.4%; Pred. No. 9.6e-35;
 Matches 118; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 3 EVOLVSGGAVPAGSLRSCASGFTPDYGMWVRQAPGKLEWVGGINNGSGTGY 62
 DB 1 QVGLQSGSELVBPASVVKLSCKASGFTFTYWMHWKQHGGLWIGNIVFGSGITNY 60
 QY 63 ADSVGRFTISRDNANKSLYLQNSLRABEDTAVYCAR-RAPIVWGQTLVTVSSGGG 121
 DB 61 DEFKKKGILTVDTSSSTAMHLSLASESAVYCARGRGLDWAGATTLTVSSGGG 120
 QY 122 SGGGSGGGGSS-ELTQ-DPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIY 179
 DB 121 SGGGSGGGGSSDIQMTSSSFVSLGDRVITICKASEDIYNRLAWYQKPGAPRLIS 180
 QY 180 GKNNRPGIDRRSGSSGNTASLTITGAQAEADYCCNRSSGNHVFEGGTULTV 238
 DB 181 GATSLGTGVRSPSGSGSDYTLTSLQTEDEVATYCCQYWSTR--TFGGGTLEI 236

RESULT 8

Q9NSD6 PRELIMINARY; PRT; 107 AA.
 ID Q9NSD6;
 AC Q9NSD6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Homo sapiens This CDS feature is included to show the translation of
 the corresponding V-region. Presently translation qualifiers on
 DE V-region features are illegal. (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocyte;
 RA Hohmann A.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: LA4092; AAA69746.2; -.
 DR FJR; S70444; S70444.
 DR HSSP: P01709; 2MCG.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 43.6%; Score 552; DB 2; Length 107;
 Best Local Similarity 98.1%; Pred. No. 3.2e-33;
 Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

134 ELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIDRRFS 193

DB 1 ELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIDRRFS 60
 QY 194 GSSSGNTASLTITGAQAEADYCCNRSSGNHVFEGGTULTVIG 240
 DB 61 GSSSGNTASLTITGAQAEADYCCNRSSGNHVFEGGTULTVIG 107

RESULT 9

Q9HCC1 PRELIMINARY; PRT; 112 AA.
 ID Q9HCC1
 AC Q9HCC1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Single chain Fv (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kikuchi M.; Takeda C.; Teujimoto Y.; Asada S.; Nagata K.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB049915; BAB16829.1; -.
 DR HSSP: P01783; 1IGC.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 112
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 43.5%; Score 550.5; DB 2; Length 112;
 Best Local Similarity 94.6%; Pred. No. 4.3e-33;
 Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVSGGAVPAGSLRSCASGFTPDYGMWVRQAPGKLEWVGGINNGSGTGY 62
 DB 1 EVOLVSGGAVPAGSLRSCASGFTPDYGMWVRQAPGKLEWVGGINNGSGTGY 60
 QY 63 ADSVGRFTISRDNANKSLYLQNSLRABEDTAVYCAR-RAPIVWGQTLV 113
 DB 61 ADSVGRFTISRDNANKSLYLQNSLRABEDTAVYCAR-RAPIVWGQTLV 112

RESULT 10

Q65ZL2 PRELIMINARY; PRT; 487 AA.
 ID Q65ZL2;
 AC Q65ZL2;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Fv/M4.
 GN Name=M4-IFN- ϵ tau>;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96272580; PubMed=8688499;
 RA Qi Y.; Xiang J.;
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
 antibody secreted from myeloma cells.";
 RL Hum. Antibodies Hybridomas 6:161-166(1995).
 DR EMBL: S82493; AAB37424.2; -.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sect; 2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
DR SEQUENCE 487 AA; 53578 MW; CTBAB69F30555504 CRC64;

Query Match 43.3%; Score 548; DB 2; Length 487;
Best Local Similarity 45.6%; Pred No. 3.3e-32;
Matches 109; Conservative 45; Mismatches 79; Indels 6; Gaps 5;

OY 2 AEVLVESGGGVRBDGSLRLSCAASGFTPDYDGMNWYRQAPGKLEWVSGINMNGSGTG 61
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:
19 SQVLQQLQSDAEIVKPGASVKISKCKASGYTFDDHAIHWAKQKPEGLIEWIGIISPENIDIX 78
OY 62 YADSVKGFPTISRDNAKNSLYIQNNLSLAEDTAYTYCARMPAPYTWGGTLVTYSRGCGG 121
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:
79 YNEKKKGATLTADSSSTAWQNLNLSIEDSAVYFCRRGRSYYG-HWGQGTTLTTS-GGGG 136
OY 122 SGGGSGGGGGGS-ELTDOPA-VSVALGTVPRTCCGDSLRSYVASWYQKPGDPAPLYTIY 179
Db 137 SGGGSGGGGGSRITQMTQSPALISVSVELVITTCASINITYSNLAWYQKQKSPQLLVY 196
OY 180 GKNNRPFGIPDRFGSSSGNTASLTITTAQADEADYYCNSRDSGSHNVVFGGKTLLV 238
Db 197 AATNLADVDPSRFSSSGGTQYSLKLNLSQESEPFSYTC-QHFVGTPYTTCGGTRLEI 253

RESULT 11
OG6MM4 PRELIMINARY; PRT; 233 AA.
OG6MM4
AC OG6MM4
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN
NM
NP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
RA Diatchenko L., Marsina K., Farmer A.S., Rubin G.M., Hong L.,
RA Stepietson M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skliss U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
NP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Straubeberg R.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

DR	EMBL: BC073786; AAH3786.1; -
DR	GO: GO:0005489; F:electron transporter activity; IEA.
DR	GO: GO:0006118; P:electron transport; IEA.
DR	InterPro: IPR003599; IG.
DR	InterPro: IPR007110; IG-like.
DR	InterPro: IPR003597; IG cl.
DR	InterPro: IPR003006; IG_MHC.
DR	InterPro: IPR003595; IG v.
DR	InterPro: IPR006662; thioRed.
DR	Pfam: PF07654; Cl-sec; 1.
DR	Pfam: PF00047; IG; 2.
DR	PRINTS: PR00421; THIOREDOXIN.
DR	SMART: SMO0409; IG; 2.
DR	SMART: SMO0407; IGcl; 1.
DR	SMART: SMO0406; IGV; 1.
DR	PROSITE: PS50835; IG_LIKE; 2.
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 233 AA; 24855 MW; 462677B3B8PDE5BD CRC64;

Query March	41.9%;	Score 530;	DB 2;	Length 233;
Best Local Similarity	91.7%;	Pred. No. 3.1e-31;		
Matches 100;	Conservative	6;	Mismatches 3;	Indels 0;
			Gaps	0

Dy	132	SSSLTDPANVSVALGQTWRIRITCOGDLSRYSYASWYQKPGAPVLVIYIKNNRPESGIDR	191
		:::::::::::::::::::::	
Dd	20	SSSLTDPANVSVALGQVTRITCOGDSLRTTYASWYQKPGAPVLVIYAKNRRPSGVDR	79
		:::::::::::::::::::::	
Oy	192	PSGGSSGNVTASLTTTGAAQEDPADYYCNSRDSGNGHVFGGKITLVIG	240
		:::::::::::::::::::::	
Dd	80	PSGGSSGNVTASLTTTGAAQEDPADYYCNSRDSGSHLVFGGITVTVIG	128
		:::::::::::::::::::::	

RESULT	12
LV3A_HUMAN	STANDARD; PRT; 108 AA.
ID	LV3A_HUMAN
AC	P01714;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
Deg	Ig lambda chain V-II region SH.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. [1]
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=7016723; PubMed=4909564;
RA	Tilani K., Wikler M., Shinoda T., Putnam P.W.;
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges.";
RT	J. Biol. Chem. 245:2171-2176(1970) .
CC	- - MISCELLANEOUS: This is a Bence-Jones protein. - - SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A01980; L3HUSH. DR HSSP; P01703; 7FAB. DR GO; GO:0005576; C:extracellular; NAS. DR GO; GO:0003823; P:antigen binding; NAS. DR GO; GO:0006955; P:immune response; NAS. DR InterPro; IPR007110; Ig-like. DR InterPro; IPR003596; Ig_v. DR Pfam; PF00047; Ig_1. DR SMART; SMO0406; IGv_1. DR PROSITE; PS50835; IG_LIKE_1. KW Bence-Jones protein; Direct protein sequencing; KW Immunoglobulin V region. FT DOMAIN 1 97 Ig-like. FT DISULFID 21 86 FT NON TER 108 108 SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;
Query Match	41.6%; Score 527; DB 1; Length 108;

ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; --.
DR HSSP; P01665; IONZ.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 40.1%; Score 507.5; DB 2; Length 218;
Best Local Similarity 47.7%; Pred. No. 1.3e-29;
Matches 102; Conservative 38; Mismatches 65; Indels 9; Gaps 4;

QY 1 MARVOLVESGGGVVRPGSLRLSCAASGFTEDDYGMGSMVRQAPGKGLGWVSGINMGSGT 60
DB 1 MAQVKLQSQSPFLKFEETVRISCKASGYFTTTAGMGMVQKMPKGLKMWGINTHSGVP 60
QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADPTAVVYCARMAP--VINGGTLVTVSR 117
DB 61 KYAEFFKGRFAFLFETASATAYLIQISNLKNEDEFTATYFCMRWDYDGFAYWGQGTIVTVSS 120
QY 118 GGGGGGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCG---DSLSTYASWYQKPG 171
DB 121 GGGGGGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFNNWFOOKPG 180
QY 172 QAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTI 205
DB 181 QPPKLIIYAASKQSGVPAGLASGSGTDFPSLNI 214

Search completed: April 25, 2005, 20:34:05
Job time : 124.991 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 3.06541 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	5	3	AAV95191
2	28	100.0	5	5	ABG78239
3	28	100.0	5	5	ABG91930
4	28	100.0	5	6	ABU11271
5	28	100.0	5	8	AD128371
6	28	100.0	10	7	ADM07746
7	28	100.0	13	7	ADM75761
8	28	100.0	13	7	ADM75496
9	28	100.0	13	7	ADM75231
10	28	100.0	13	7	ADM75760
11	28	100.0	13	7	ADM74966
12	28	100.0	13	7	ADM74967
13	28	100.0	14	8	ABM79481
14	28	100.0	16	2	AA849460
15	28	100.0	20	5	ABU05002
16	28	100.0	26	1	ABF61435
17	28	100.0	29	1	AAFS0314
18	28	100.0	33	1	AAFS0318
19	28	100.0	41	1	AAFS0313
20	28	100.0	60	5	ABJ04948
21	28	100.0	73	3	AA807206
22	28	100.0	98	3	AA840073
23	28	100.0	98	5	ABG78186
24	28	100.0	98	5	ABG91877
25	28	100.0	98	6	ABO27087

26	28	100.0	98	7	ADP09916
27	28	100.0	98	7	ADP10126
28	28	100.0	98	7	ADP10024
29	28	100.0	98	7	ADJ80300
30	28	100.0	113	3	AAV95177
31	28	100.0	113	3	AAV95178
32	28	100.0	115	3	AAV95189
33	28	100.0	115	3	AAV95190
34	28	100.0	116	2	AAW19880
35	28	100.0	117	2	AA866312
36	28	100.0	118	4	AAU02560
37	28	100.0	120	2	AA825204
38	28	100.0	123	8	ADJ57861
39	28	100.0	207	5	AAU98019
40	28	100.0	211	1	AA850091
41	28	100.0	211	3	AA807203
42	28	100.0	214	3	AA838412
43	28	100.0	232	7	ABO62069
44	28	100.0	235	8	ADR28086
45	28	100.0	236	3	AA829486

ALIGNMENTS

RESULT 1
ID AAV95191 standard; peptide; 5 AA.
AC AAV95191;
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein IB human H1B-1 VH CDR1.
XX
KW Variable heavy chain; single chain antibody; scFv; human; H1B-1;
KW glycoprotein IB alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR1;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025495.
XX
PR 30-OCT-1998; 98US-0106275P.
XX
PA (MILLER) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
PT IB alpha molecule useful for producing antibodies which inhibit platelet
PT aggregation.
XX
PS Claim 14; Fig 5; 89pp; English.
XX
CC The present sequence is that of complementarity determining region 1
CC (CDR1) of the heavy chain variable region (VH) of human single chain
CC antibody (scFv) H1B-1 (see AAV95198), which is directed against platelet
CC glycoprotein IB (GP1b). The H1B series of scFv was isolated from a human
CC synthetic VH and VL scFv library on the basis of their binding to
CC platelet GP1b. Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by *Escherichia coli*, the H1B scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences and
CC are therefore attractive potential reagents for therapeutic purposes.
CC They provide a new class of antithrombotic agents, useful for the

CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIIb/IIIa and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL
 CC chain, including CDR fragments, are also claimed

XX Sequence 5 AA;

Query Match 100.0%; Score 28; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 DB 1 DYGMS 5

RESULT 2

ID ABG78239 standard; peptide; 5 AA.

AC ABG78239;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule; hypervariable region related peptide #114.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.

OS Homo sapiens.

PN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

PR 29-DEC-2000; 2000US-00751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

PI Plakstein D, Peretz T;

DR WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

PS Claim 20; Page 208; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or a fragment of a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has actively against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 28; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 DB 1 DYGMS 5

RESULT 3

ID ABG91930 standard; peptide; 5 AA.

AC ABG91930;

DT 04-DEC-2002 (first entry)

DE Human antibody fragment #114.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;

KW restenosis; leukemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plakstein D, Vogel T, Nimrod A, Mar-Haim H;

PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

DR WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

PS Claim 25; Page 284; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody.
 CC Its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukemia cells, increase in number of tumour or leukemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukemia agents, or for decreasing the number of tumour or leukemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

XX

SQ Sequence 5 AA;
 Query Match 100.0%; Score 28; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 1 DYGMS 5
 RESULT 4
 ABU1271
 ID ABU1271 standard; peptide; 5 AA.
 XX
 AC ABU1271;
 DT 06-FEB-2003 (first entry)
 XX
 DE Human TANGO 268 VHCDR1 Peptide #5.
 XX
 KM Human; mouse; variable heavy; VH; antigen; cancer;
 KM complementarity determining region; TANGO 268; glycoprotein VI; GPII;
 KM TANGO 268; extracellular matrix; collagen; platelet release;
 KM proliferation; migration; embryogenesis; inflammation; thrombosis;
 KM degranulation; thrombocytopenia; antibody; thrombotic disorder;
 KM cerebral vascular disease; stroke; ischemia; venous thromboembolism;
 KM leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KM cardiovascular disease; angina pectoris; myocardial infarction;
 KM coronary restenosis; atherosclerosis; immunological disorder;
 KM developmental disorder; embryonic disorder; liver disorder;
 KM cerebral vascular disease; venous thromboembolism disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200280968-A1.
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US011122.
 XX
 PR 09-APR-2001; 2001US-00829495.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Bugfield SJ, Villeva J, Jandrot-Perrus M, Vainchenker W,
 PI Gill DS, Qian DM, Kingsbury G;
 XX
 DR WPI; 2003-058477/05.
 XX
 PT Novel substantially purified antibody immunospecifically binding to TANGO
 PT 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
 XX
 PS Claim 1; Page 11; 236pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPII)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268
 CC binding to extracellular matrix components, or as a Collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.

CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina,
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 28; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 1 DYGMS 5
 RESULT 5
 ADI28371
 ID ADI28371 standard; peptide; 5 AA.
 XX
 AC ADI28371;
 DT 06-MAY-2004 (first entry)
 XX
 DE Human CDR1 peptide, used in therapeutic composition.
 XX
 KM Human; antibody; scFv; complementarity determining region; drug delivery;
 KM cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020604.
 XX
 PR 01-JUL-2002; 2002US-00189025.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 PI WPI; 2004-099189/10.
 XX
 DR Composition comprising an agent and/or antibody or its fragment, useful
 DR for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 DR PT for inhibiting growth and/or replication of tumor cells or leukemia
 DR cells.
 XX
 PS Claim 15; SEQ ID NO 6; 56pp; English.
 XX
 CC The present sequence is that of a human antibody complementarity
 CC determining region 1 (CDR1). The invention relates to compositions
 CC utilising an agent and an antibody or its fragment. The agent is a toxin,
 CC radioisotope or pharmaceutical agent such as doxorubicin. It is complexed
 CC or combined with or conjugated to the antibody or its fragment. The
 CC antibody may have a first hypervariable region comprising a CDR3, a
 CC second hypervariable region comprising a CDR2 and a third hypervariable
 CC sequence comprising the present CDR1 sequence. The agent and/or antibody
 CC can be present in the composition is a sub-clinical amount, i.e. less
 CC than the amount generally found to be clinically effective when the agent
 CC is administered alone. The composition is used in claimed methods of:
 CC inhibiting cell rolling, inflammation, thrombosis, restenosis,
 CC metastasis, the growth and/or replication of tumour cells or leukaemia
 CC cells, an increase in number of tumour or leukaemia cells, cell-cell,

CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet
 CC complex formation, aggregation or adhesion; increasing the mortality rate
 CC of tumour or leukaemia cells, the susceptibility of disease cells to
 CC damage by anti-disease agents, and the susceptibility of tumour or
 CC leukaemia cells to damage by anti-cancer agents; and ameliorating the
 CC effects of a disease, preventing a disease, treating a disease or
 CC inhibiting the progress of a disease.

XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 28; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYCGMS 5
 |||||
 Db 1 DYCGMS 5

RESULT 6

ADM07746
 ID ADM07746 standard; peptide; 10 AA.

AC ADM07746;

DT 20-MAY-2004 (first entry)

XX Canine immunoglobulin heavy chain variable domain CDR1 peptide 14.

XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KW antiallergic; allergy; IgE; gene therapy;

KM complementarity determining region; CDR1.

OS Canis familiaris.

XX WO2003060080-A2.

PD 24-JUL-2003.

XX 20-DEC-2002; 2002WO-US041362.

XX 21-DEC-2001; 2001US-0344874P.

PI (INDEX-) IDEXX LAB INC.

XX Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

XX New canine heavy and light chain variable domain polypeptides, useful for

PT treating canine allergy.

XX Claim 15; Page 95; 130pp; English.

XX The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,

CC possibly via gene therapy. The current sequence is that of a canine

CC immunoglobulin heavy chain variable domain complementarity determining

CC region (CDR) peptide of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 28; DB 7; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.2; Indels 0; Gaps 0;

OY 1 DYCGMS 5
 |||||
 Db 6 DYCGMS 10

RESULT 7

ADM75761
 ID ADM75761 standard; peptide; 13 AA.

XX ADM75761;

DT 03-JUN-2004 (first entry)

XX Potential human MHC class II binding human Factor VIII peptide #981.

XX human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;

KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

OS Homo sapiens.

XX WO2003087161-A1.

PD 23-OCT-2003.

XX 17-APR-2003; 2003WO-EP04063.

XX 18-APR-2002; 2002EP-00008712.

XX 24-MAR-2003; 2003EP-00006554.

XX (MERE) MERCK PATENT GMBH.

XX Jones T, Baker M, Carr FJ;

DR WPI; 2003-845307/78.

XX New modified human Factor VIII molecule being substantially non-

PT immunogenic or less immunogenic than non-modified human Factor VIII,

PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX Disclosure; Fig 1; 68pp; English.

XX The invention relates to a novel modified human Factor VIII molecule. The

CC modified human Factor VIII molecule being substantially non-immunogenic

CC or less immunogenic than a non-modified human Factor VIII and having

CC essentially the same biological specificity and activity when used in

CC vivo. The modified human Factor VIII molecule comprises specifically

CC altered amino acid residues compared with the non-modified parental

CC molecule, where the altered amino acid residues cause a reduction or an

CC elimination of one or more of the T-cell epitopes, which act in the

CC parental non-modified molecule as MHC class II binding ligands and

CC stimulate T-cells. The potential MHC class II binding activity peptide is

CC useful for the manufacture of the modified Factor VIII molecule or a

CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.

CC The modified Factor VIII molecule is useful in preparing a composition

CC for treating e.g., Gaucher's disease. This sequence represents a human

CC Factor VIII peptide with potential human MHC class II binding activity of

XX the invention.

RESULT 8

ADM75496
 ID ADM75496 standard; peptide; 13 AA.

XX ADM75496;

DT 03-JUN-2004 (first entry)

XX Potential human MHC class II binding human Factor VIII peptide #716.

KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX
 OS Homo sapiens.
 PN WO2003087161-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 17-APR-2003; 2003WO-EP004063.
 XX
 PR 18-APR-2002; 2002EP-00008712.
 PR 24-MAR-2003; 2003EP-00006554.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Jones T, Baker M, Carr FJ;
 DR WPI; 2003-845307/78.
 XX
 PT New modified human Factor VIII molecule being substantially non-
 immunogenic or less immunogenic than non-modified human Factor VIII,
 useful in preparing a composition for treating e.g., Gaucher's disease.
 XX
 PS Disclosure; Fig 1; 68pp; English.
 XX
 CC The invention relates to a novel modified human Factor VIII molecule. The
 modified human Factor VIII molecule being substantially non-immunogenic
 or less immunogenic than a non-modified human Factor VIII and having
 essentially the same biological specificity and activity when used in
 vivo. The modified human Factor VIII molecule comprises specifically
 altered amino acid residues compared with the non-modified parental
 molecule, where the altered amino acid residues cause a reduction or an
 elimination of one or more of the T-cell epitopes, which act in the
 parental non-modified molecule as MHC class II binding ligands and
 stimulate T-cells. The potential MHC class II binding activity peptide is
 useful for the manufacture of the modified Factor VIII molecule or a
 vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 for treating e.g., Gaucher's disease. This sequence represents a human
 Factor VIII peptide with potential human MHC class II binding activity of
 the invention.
 CC
 CC
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 |||||
 Db 4 DYGMS 8
 XX
 RESULT 9
 ADM75231
 ID ADM75231 standard; peptide; 13 AA.
 XX
 AC ADM75231;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Potential human MHC class II binding human Factor VIII peptide #451.
 XX
 KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX
 OS Homo sapiens.
 PN WO2003087161-A1.
 XX
 PD 23-OCT-2003.
 XX

PF 17-APR-2003; 2003WO-EP004063.
 XX
 PR 18-APR-2002; 2002EP-00008712.
 PR 24-MAR-2003; 2003EP-00006554.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Jones T, Baker M, Carr FJ;
 DR WPI; 2003-845307/78.
 XX
 PT New modified human Factor VIII molecule being substantially non-
 immunogenic or less immunogenic than non-modified human Factor VIII,
 useful in preparing a composition for treating e.g., Gaucher's disease.
 XX
 PS Disclosure; Fig 1; 68pp; English.
 XX
 CC The invention relates to a novel modified human Factor VIII molecule. The
 modified human Factor VIII molecule being substantially non-immunogenic
 or less immunogenic than a non-modified human Factor VIII and having
 essentially the same biological specificity and activity when used in
 vivo. The modified human Factor VIII molecule comprises specifically
 altered amino acid residues compared with the non-modified parental
 molecule, where the altered amino acid residues cause a reduction or an
 elimination of one or more of the T-cell epitopes, which act in the
 parental non-modified molecule as MHC class II binding ligands and
 stimulate T-cells. The potential MHC class II binding activity peptide is
 useful for the manufacture of the modified Factor VIII molecule or a
 vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 for treating e.g., Gaucher's disease. This sequence represents a human
 Factor VIII peptide with potential human MHC class II binding activity of
 the invention.
 CC
 CC
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 |||||
 Db 5 DYGMS 9
 XX
 RESULT 10
 ADM75760
 ID ADM75760 standard; peptide; 13 AA.
 XX
 AC ADM75760;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Potential human MHC class II binding human Factor VIII peptide #980.
 XX
 KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX
 OS Homo sapiens.
 PN WO2003087161-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 17-APR-2003; 2003WO-EP004063.
 XX
 PR 18-APR-2002; 2002EP-00008712.
 PR 24-MAR-2003; 2003EP-00006554.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Jones T, Baker M, Carr FJ;
 XX

DR WPI, 2003-845307/78.

XX New modified human Factor VIII molecule being substantially non-
PT immunogenic or less immunogenic than non-modified human Factor VIII,
PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX Disclosure; Fig 1; 68pp; English.

PS The invention relates to a novel modified human Factor VIII molecule. The
CC modified human Factor VIII molecule being substantially non-immunogenic
CC or less immunogenic than a non-modified human Factor VIII and having
CC essentially the same biological specificity and activity when used in
CC vivo. The modified human Factor VIII molecule comprises specifically
CC altered amino acid residues compared with the non-modified parental
CC molecule, where the altered amino acid residues cause a reduction or an
CC elimination of one or more of the T-cell epitopes, which act in the
CC parental non-modified molecule as MHC class II binding ligands and
CC stimulate T-cells. The potential MHC class II binding activity peptide is
CC useful for the manufacture of the modified Factor VIII molecule or a
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC The modified Factor VIII molecule is useful in preparing a composition
CC for treating e.g., Gaucher's disease. This sequence represents a human
CC Factor VIII peptide with potential human MHC class II binding activity of
CC the invention.

CC Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5

DB 9 DYGM5 13

RESULT 11

ADM74966 standard; peptide; 13 AA.

XX ADM74966;

XX 03-JUN-2004 (first entry)

XX Potential human MHC class II binding human Factor VIII peptide #186.

KM human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

OS Homo sapiens.

XX WO2003087161-A1.

XX 23-OCT-2003.

XX 17-APR-2003; 2003WO-EP004063.

XX 18-APR-2002; 2002EP-00008712.

XX 24-MAR-2003; 2003EP-00006554.

XX (MERCK) MERCK PATENT GMBH.

XX Jones T, Baker M, Carr FJ;

XX WPI, 2003-845307/78.

PT New modified human Factor VIII molecule being substantially non-
PT immunogenic or less immunogenic than non-modified human Factor VIII,
PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX Disclosure; Fig 1; 68pp; English.

CC The invention relates to a novel modified human Factor VIII molecule. The

CC modified human Factor VIII molecule being substantially non-immunogenic
CC or less immunogenic than a non-modified human Factor VIII and having
CC essentially the same biological specificity and activity when used in
CC vivo. The modified human Factor VIII molecule comprises specifically
CC altered amino acid residues compared with the non-modified parental
CC molecule, where the altered amino acid residues cause a reduction or an
CC elimination of one or more of the T-cell epitopes, which act in the
CC parental non-modified molecule as MHC class II binding ligands and
CC stimulate T-cells. The potential MHC class II binding activity peptide is
CC useful for the manufacture of the modified Factor VIII molecule or a
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC The modified Factor VIII molecule is useful in preparing a composition
CC for treating e.g., Gaucher's disease. This sequence represents a human
CC Factor VIII peptide with potential human MHC class II binding activity of
CC the invention.

CC Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5

DB 8 DYGM5 12

RESULT 12

ADM74967 standard; peptide; 13 AA.

XX ADM74967;

XX 03-JUN-2004 (first entry)

XX Potential human MHC class II binding human Factor VIII peptide #187.

KM human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

OS Homo sapiens.

XX WO2003087161-A1.

XX 23-OCT-2003.

XX 17-APR-2003; 2003WO-EP004063.

XX 18-APR-2002; 2002EP-00008712.

XX 24-MAR-2003; 2003EP-00006554.

XX (MERCK) MERCK PATENT GMBH.

XX Jones T, Baker M, Carr FJ;

XX WPI, 2003-845307/78.

PT New modified human Factor VIII molecule being substantially non-
PT immunogenic or less immunogenic than non-modified human Factor VIII,
PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX Disclosure; Fig 1; 68pp; English.

CC The invention relates to a novel modified human Factor VIII molecule. The
CC modified human Factor VIII molecule being substantially non-immunogenic
CC or less immunogenic than a non-modified human Factor VIII and having
CC essentially the same biological specificity and activity when used in
CC vivo. The modified human Factor VIII molecule comprises specifically
CC altered amino acid residues compared with the non-modified parental
CC molecule, where the altered amino acid residues cause a reduction or an
CC elimination of one or more of the T-cell epitopes, which act in the
CC parental non-modified molecule as MHC class II binding ligands and
CC stimulate T-cells. The potential MHC class II binding activity peptide is

CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.

XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 DB 2 DYGMS 6

RESULT 13

ABM79481
 ID ABM79481 standard; peptide; 14 AA.

XX
 AC ABM79481;

XX
 DT 22-APR-2004 (first entry)

XX
 DE Human Factor VIII peptide fragment SEQ ID NO: 5.

XX
 KM Antibody; human; Factor VIII; LRP; haemostatic; haemophilia A;

XX
 KM low-density lipoprotein receptor-related protein;

XX
 KM blood coagulation disorder.

OS Homo sapiens.

XX
 PN WO2003093313-A2.

XX
 PD 13-NOV-2003.

XX
 PF 28-APR-2003; 2003WO-EP004425.

XX
 PR 29-APR-2002; 2002US-0376351P.

XX
 PA (BAXT) BAXTER INT INC.

XX
 PA (BAXT) BAXTER HEALTHCARE SA.

XX
 PI (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX
 PI Mertens K, Bovenschen AN, Voorberg J, Rieger M, Scheiflinger F;

XX
 DR WPI; 2004-053039/05.

XX
 PT Use of peptides derived from and antibodies generated against Factor VIII
 PT to inhibit Factor VIII interaction with Low Density Lipoprotein Receptor
 PT protein or to prevent or treat blood coagulation disorders (e.g.
 PT hemophilia A).

XX
 PS Example 1; Page 49; Opp; English.

XX
 CC The present invention relates to peptides derived from Factor VIII but
 CC not having any substantial Factor VIII activity, or an antibody which
 CC specifically binds to epitopes within the amino acid sequences, which can
 CC be used to inhibit Factor VIII interaction with Low Density Lipoprotein
 CC Receptor Protein (LRP). The peptides or antibody are useful in inhibiting
 CC Factor VIII interaction with LRP, in decreasing Factor VIII degradation
 CC in a biological fluid, in prolonging Factor VIII half-life in blood or in
 CC preparing a medicament for preventing or treating a blood coagulation
 CC disorder (e.g. haemophilia A or von Willebrand's disease) and/or a
 CC temporary impairment of the thrombolytic or fibrinolytic systems. The
 CC present sequence is a polypeptide shown in the exemplification of the
 CC invention

XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 28; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 DB 2 DYGMS 6

RESULT 14

AAR49460
 ID AAR49460 standard; protein; 16 AA.

XX
 AC AAR49460;

XX
 DT 25-MAR-2003 (revised)

XX
 DT 16-SEP-1994 (first entry)

XX
 DE Factor VIII position 1175-1790.

XX
 KM Naturally-occurring immunomodulatory protein; human; therapy; class I;

XX
 KM major histocompatibility complex; class II; allotype; type I diabetes;

XX
 KM autoimmune disease; rheumatoid arthritis; T-cell-mediated response;

XX
 KM multiple sclerosis; transplant rejection; vaccine; MHC.

OS Homo sapiens.

XX
 PN WO9404171-A1.

XX
 PD 03-MAR-1994.

XX
 PF 11-AUG-1993; 93WO-US007545.

XX
 PR 11-AUG-1992; 92US-00925460.

XX
 PR 15-JUN-1993; 93US-00077255.

XX
 PA (HARD) HARVARD COLLEGE.

XX
 PI Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;

XX
 PI Strominger JL;

XX
 DR WPI; 1994-082825/10.

XX
 PT Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT treatment of autoimmune diseases, transplant rejection and for
 PT vaccination.

XX
 PS Disclosure; Page 41; 139pp; English.

XX
 CC The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
 CC fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human major
 CC histocompatibility complex (MHC) class II allotype. These peptides may be
 CC used for therapy of autoimmune diseases, such as type I diabetes,
 CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant
 CC rejection. They may also be used for vaccination providing an exclusively
 CC T-cell-mediated response, which can be class I or class-II based, or
 CC both, depending on the length and character of the immunogenic peptides.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)

XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 28; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 DB 3 DYGMS 7

RESULT 15

ABJ05002

ID ABJ05002 standard; peptide; 20 AA.
 XX
 AC ABJ05002;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE A3 peptide of FVII precursor SEQ ID No 58.
 XX
 KM Haemostatic; antibody inhibitor; factor VIII; T cell; immune response;
 XX haemophilia A; acquired haemophilia; human factor VIII.
 OS Homo sapiens.
 XX
 PN W0200260917-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-NOV-2001; 2001WO-US044945.
 XX
 PR 01-DEC-2000; 2000US-0250430P.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Conti-Fine BM;
 XX
 DR WPI; 2002-627462/67.
 XX
 PT New peptides or their variants, useful for preventing, treating or
 PT inhibiting aberrant or pathogenic production of antibodies specific for
 PT factor VIII, particularly useful for treating hemophilia A or acquired
 PT hemophilia.
 XX
 PS Claim 44; Page 62; 120P; English.
 XX

CC The invention relates to isolated and purified peptides and variants
 CC thereof, as well as DNA encoding those peptides, useful to prevent or
 CC treat antibody inhibitors of factor VIII. The peptides are useful for
 CC preventing or inhibiting aberrant, pathogenic or undesirable antibody
 CC production or antibody binding that is specific for factor VIII. The
 CC peptides are also useful for preventing or inhibiting the priming or
 CC activity of T cells specific for factor VIII. These peptides are also
 CC useful for enhancing the activity or increasing the levels of modulatory
 CC T cells that inhibit the immune response to factor VIII. These peptides
 CC are useful in mammals, particularly in humans. The administration of
 CC these peptides does not increase the synthesis of a pathogenic antibody
 CC to factor VIII, or its biologically active fragment or functional
 CC equivalent. In particular, these peptides are useful for treating
 CC haemophilia A or acquired haemophilia. This sequence represents a human
 CC factor VIII peptide region relating to the invention
 CC
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 28; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYGM5 5
 |||||
 Db 9 DYGM5 13

Search completed: April 25, 2005, 20:22:28
 Job time : 5.06541 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 0.77051 Seconds

(without alignments)
484,413 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/pcodata/1/1aa/5A COMB .pep.*
2: /cgn2_6/pcodata/1/1aa/5B COMB .pep.*
3: /cgn2_6/pcodata/1/1aa/6A COMB .pep.*
4: /cgn2_6/pcodata/1/1aa/6B COMB .pep.*
5: /cgn2_6/pcodata/1/1aa/PTUS COMB .pep.*
6: /cgn2_6/pcodata/1/1aa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	16	2 US-08-480-190-170	Sequence 170, App
2	28	100.0	16	2 US-08-488-379-170	Sequence 170, App
3	28	100.0	16	4 US-08-475-399A-170	Sequence 170, App
4	28	100.0	16	4 US-08-077-255A-170	Sequence 170, App
5	28	100.0	16	5 PCT-US93-07545-170	Sequence 170, App
6	28	100.0	116	2 US-08-652-816A-14	Sequence 14, Appl
7	28	100.0	117	3 US-08-545-809A-106	Sequence 106, App
8	28	100.0	232	4 US-09-489-039A-8586	Sequence 8586, App
9	28	100.0	258	4 US-09-107-532A-4002	Sequence 4002, App
10	28	100.0	254	4 US-09-107-532A-6813	Sequence 6813, App
11	28	100.0	309	3 US-09-079-029-9	Sequence 9, Appl1
12	28	100.0	334	3 US-08-724-984A-2	Sequence 2, Appl1
13	28	100.0	373	4 US-09-828-995B-35	Sequence 35, Appl1
14	28	100.0	470	4 US-09-828-995B-11	Sequence 11, Appl1
15	28	100.0	474	4 US-09-486-192-4	Sequence 4, Appl1
16	28	100.0	520	4 US-09-902-540-11365	Sequence 11365, A
17	28	100.0	868	1 US-07-864-004B-6	Sequence 6, Appl1
18	28	100.0	868	1 US-08-251-937A-6	Sequence 6, Appl1
19	28	100.0	868	1 US-08-212-133A-3	Sequence 6, Appl1
20	28	100.0	1090	5 PCT-US93-03275-6	Sequence 6, Appl1
21	28	100.0	1438	3 US-09-209-916-1	Sequence 1, Appl1
22	28	100.0	1443	2 US-08-670-707A-39	Sequence 39, Appl1
23	28	100.0	1443	3 US-09-037-601-39	Sequence 39, Appl1
24	28	100.0	1443	3 US-09-315-179-39	Sequence 39, Appl1
25	28	100.0	1457	4 US-09-001-039B-47	Sequence 47, Appl1
26	28	100.0	1467	4 US-09-523-656-38	Sequence 38, Appl1
27	28	100.0	1471	1 US-08-663-839B-3	Sequence 3, Appl1

28	28	100.0	1661	2 US-08-882-083-2	Sequence 2, Appl1
29	28	100.0	1661	2 US-08-558-107-2	Sequence 2, Appl1
30	28	100.0	1661	3 US-09-243-539-2	Sequence 2, Appl1
31	28	100.0	2115	3 US-09-324-867-5	Sequence 5, Appl1
32	28	100.0	2133	2 US-08-670-707A-37	Sequence 37, Appl1
33	28	100.0	2133	3 US-09-037-601-37	Sequence 37, Appl1
34	28	100.0	2133	3 US-09-315-179-37	Sequence 37, Appl1
35	28	100.0	2133	4 US-09-523-656-30	Sequence 30, Appl1
36	28	100.0	2304	3 US-09-324-867-4	Sequence 4, Appl1
37	28	100.0	2319	1 US-08-212-133A-8	Sequence 8, Appl1
38	28	100.0	2319	1 US-08-474-503-6	Sequence 6, Appl1
39	28	100.0	2319	2 US-08-670-707A-6	Sequence 6, Appl1
40	28	100.0	2319	3 US-09-037-601-6	Sequence 6, Appl1
41	28	100.0	2319	3 US-09-315-179-6	Sequence 28, Appl1
42	28	100.0	2319	4 US-09-523-656-28	Sequence 28, Appl1
43	28	100.0	2319	5 PCT-US94-13200-6	Sequence 6, Appl1
44	28	100.0	2332	1 US-07-864-004B-4	Sequence 4, Appl1
45	28	100.0	2332	1 US-08-251-937A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-480-190-170

; Sequence 170, Application US/08480190

; Patent No. 5827516

; GENERAL INFORMATION:

; APPLICANT: Robert G. Urban

; APPLICANT: Roman M. Chicz

; APPLICANT: Darío A. A. Vignali

; APPLICANT: Mary L. Hedley

; APPLICANT: Lawrence J. Stern

; APPLICANT: Jack L. Ströminger

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 555X

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,190

; FILING DATE: 424

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/077,255

; FILING DATE: June 15, 1993

; APPLICATION NUMBER: 07/925,460

; FILING DATE: August 11, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00246/168001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 170:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-480-190-170

Query Match 100.0%; Score 28; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
|||||
Db 3 DYGM 7

RESULT 2
US-08-488-379-170
; Sequence 170, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-170

Query Match 100.0%; Score 28; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
|||||
Db 3 DYGM 7

RESULT 3
US-08-475-399A-170
; Sequence 170, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-475-399A-170

Query Match 100.0%; Score 28; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
|||||
Db 3 DYGM 7

RESULT 4
US-08-077-255A-170
; Sequence 170, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-077-255A-170

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-170

Query Match 100.0%; Score 28; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 3 DYGMS 7

RESULT 5
PCT-US93-07545-170
Sequence 170, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strömberg
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-170

Query Match 100.0%; Score 28; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 3 DYGMS 7

RESULT 6
US-08-652-816A-14
Sequence 14, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
NUMBER OF SEQUENCES: 53
TITLE OF INVENTION: methods.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-14

Query Match 100.0%; Score 28; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 31 DYGMS 35

RESULT 7
US-08-545-809A-106
Sequence 106, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tsauku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-106

Query Match 100.0%; Score 28; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 50 DYGMS 54

RESULT 8
US-09-489-039A-8586
Sequence 8586, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8586
LENGTH: 232
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8586

Query Match 100.0%; Score 28; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 219 DYGMS 223

RESULT 9
US-09-107-532A-4002
Sequence 4002, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 4002:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...258
SEQUENCE DESCRIPTION: SEQ ID NO: 4002
US-09-107-532A-4002

Query Match 100.0%; Score 28; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5
DB 172 DYGS 176

RESULT 10
US-09-107-532A-6813
Sequence 6813 Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6813:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...264
SEQUENCE DESCRIPTION: SEQ ID NO: 6813;
US-09-107-532A-6813

Query Match 100.0%; Score 28; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5
DB 178 DYGS 182

RESULT 11
US-09-079-029-9
Sequence 9 Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntarapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9681
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-079-029-9

Query Match 100.0%; Score 28; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5
DB 70 DYGS 74

RESULT 12
US-08-724-984A-2
Sequence 2 Application US/08724984A
Patent No. 6388055
GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawer, and Usman Shabon
TITLE OF INVENTION: No. 63880551 Mouse Genomic Clone of the CC-
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A

```

; FILING DATE: October 3, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-724-984A-2

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```

Query Match          100.0%; Score 28; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DYGM5 5
Db 15 DYGM5 19

```

```

RESULT 13
US-09-828-995B-35
; Sequence 35, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heeka Corporation
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-35.

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Query Match          100.0%; Score 28; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 DYGM5 5
Db 50 DYGM5 54

```

```

RESULT 14
US-09-828-995B-11
; Sequence 11, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heeka Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09

```

```

; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-11

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Query Match          100.0%; Score 28; DB 4; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYGM5 5
Db 50 DYGM5 54

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```

RESULT 15
US-09-486-192-4
; Sequence 4, Application US/09486192
; Patent No. 6521440
; GENERAL INFORMATION:
; APPLICANT: Betell, David A.
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC386-US
; CURRENT APPLICATION NUMBER: US/09/486,192
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US98/18677
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: EP9719637.2
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-486-192-4

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Query Match          100.0%; Score 28; DB 4; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYGM5 5
Db 349 DYGM5 353

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Search completed: April 25, 2005, 21:12:13
Job time : 0.77051 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 2.21175 Seconds
(without alignments)
752.325 Million cell updates/sec

Title: US-10-029-926d-114

Perfect score: 28
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	5	9 US-09-832-312-73	Sequence 73, Appl
2	28	100.0	5	11 US-09-829-495-73	Sequence 73, Appl
3	28	100.0	5	15 US-10-032-037B-114	Sequence 114, Appl
4	28	100.0	5	15 US-10-029-988B-114	Sequence 114, Appl
5	28	100.0	5	15 US-10-032-423A-114	Sequence 114, Appl
6	28	100.0	5	15 US-10-029-926B-114	Sequence 114, Appl
7	28	100.0	10	16 US-10-327-598-445	Sequence 445, Appl
8	28	100.0	20	15 US-10-433-273-58	Sequence 58, Appl
9	28	100.0	60	15 US-10-433-273-4	Sequence 4, Appl
10	28	100.0	60	15 US-10-194-975-20	Sequence 20, Appl
11	28	100.0	98	15 US-10-308-817-60	Sequence 60, Appl
12	28	100.0	98	15 US-10-032-037B-61	Sequence 61, Appl
13	28	100.0	98	15 US-10-029-988B-61	Sequence 61, Appl

14	28	100.0	98	15	US-10-032-423A-61	Sequence 61, Appl
15	28	100.0	98	15	US-10-453-698-60	Sequence 60, Appl
16	28	100.0	98	15	US-10-029-926B-61	Sequence 61, Appl
17	28	100.0	98	16	US-10-379-393-21	Sequence 21, Appl
18	28	100.0	98	16	US-10-884-830-559	Sequence 559, Appl
19	28	100.0	116	16	US-10-437-963-114282	Sequence 114282, Appl
20	28	100.0	156	16	US-10-424-599-215325	Sequence 215325, Appl
21	28	100.0	239	10	US-09-880-748-937	Sequence 937, Appl
22	28	100.0	239	10	US-09-880-748-2015	Sequence 2015, Appl
23	28	100.0	239	10	US-09-880-748-2038	Sequence 2038, Appl
24	28	100.0	239	15	US-10-293-418-937	Sequence 937, Appl
25	28	100.0	239	15	US-10-293-418-2015	Sequence 2015, Appl
26	28	100.0	239	15	US-10-293-418-2038	Sequence 2038, Appl
27	28	100.0	242	17	US-10-935-290-130	Sequence 130, Appl
28	28	100.0	244	14	US-10-322-673-42	Sequence 42, Appl
29	28	100.0	249	17	US-10-935-290-40	Sequence 40, Appl
30	28	100.0	251	10	US-09-880-748-1542	Sequence 1542, Appl
31	28	100.0	251	15	US-10-293-418-1542	Sequence 1542, Appl
32	28	100.0	266	15	US-10-032-037B-204	Sequence 204, Appl
33	28	100.0	266	15	US-10-029-988B-204	Sequence 204, Appl
34	28	100.0	266	15	US-10-032-423A-204	Sequence 204, Appl
35	28	100.0	276	15	US-10-425-114-70003	Sequence 70003, Appl
36	28	100.0	277	15	US-10-032-037B-25	Sequence 25, Appl
37	28	100.0	277	15	US-10-032-037B-203	Sequence 203, Appl
38	28	100.0	277	15	US-10-029-988B-25	Sequence 25, Appl
39	28	100.0	277	15	US-10-029-988B-203	Sequence 203, Appl
40	28	100.0	277	15	US-10-032-423A-25	Sequence 25, Appl
41	28	100.0	277	15	US-10-032-423A-203	Sequence 203, Appl
42	28	100.0	277	15	US-10-029-926B-25	Sequence 25, Appl
43	28	100.0	277	15	US-10-029-926B-203	Sequence 203, Appl
44	28	100.0	279	15	US-10-425-114-36951	Sequence 36951, Appl
45	28	100.0	299	16	US-10-767-701-44522	Sequence 44522, Appl

ALIGNMENTS

RESULT 1
US-09-832-312-73
; Sequence 73, Application US/09832312
; Patent No. US20010049629A1
; GENERAL INFORMATION:
; APPLICANT: Buefield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-73

Query Match 100.0%; Score 28; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 DYGMS 5
Db 1 DYGMS 5

RESULT 2

```
US-09-829-495-73
; Sequence 73, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villaveal J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Valinckx W
; APPLICANT: Gail DS
; APPLICANT: Olan MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-73
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Query Match          100.0%; Score 28; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DYGS 5
Db 1 DYGS 5
```

```
RESULT 3
US-10-032-037B-114
; Sequence 114, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-114
```

```
Query Match          100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DYGS 5
Db 1 DYGS 5
```

```
RESULT 4
US-10-029-988B-114
; Sequence 114, Application US/10029988B
; Publication No. US20040001839A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-114
```

```
Query Match          100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DYGS 5
Db 1 DYGS 5
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```
RESULT 5
US-10-032-423A-114
; Sequence 114, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-114
```

```
Query Match          100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DYGS 5
Db 1 DYGS 5
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```
RESULT 6
US-10-029-926B-114
; Sequence 114, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
```


ORGANISM: Homo sapiens
US-10-029-926d-114

Query Match 100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 1 DYGMS 5

RESULT 7

US-10-327-598-445
Sequence 445, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Hongliang
APPLICANT: Alivappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 445
LENGTH: 10
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-445

Query Match 100.0%; Score 28; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 6 DYGMS 10

RESULT 8

US-10-433-273-58
Sequence 58, Application US/10433273
Publication No. US20040096456A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
APPLICANT: Conti-Fine, Bianca M.
TITLE OF INVENTION: Methods to Treat Hemophilia
FILE REFERENCE: 600.507M01
CURRENT APPLICATION NUMBER: US/10/433,273
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 60/250,430
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 58
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-433-273-58

Query Match 100.0%; Score 28; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 9 DYGMS 13

RESULT 9

US-10-433-273-4
Sequence 4, Application US/10433273
Publication No. US20040096456A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
APPLICANT: Conti-Fine, Bianca M.
TITLE OF INVENTION: Methods to Treat Hemophilia
FILE REFERENCE: 600.507M01
CURRENT APPLICATION NUMBER: US/10/433,273
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 60/250,430
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 4
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-10-433-273-4

Query Match 100.0%; Score 28; DB 15; Length 60;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 39 DYGMS 43

RESULT 10

US-10-194-975-20
Sequence 20, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-20

Query Match 100.0%; Score 28; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 31 DYGMS 35

RESULT 11

US-10-308-817-60
Sequence 60, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Roeder, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60

LENGTH: 98
TYPE: PRT
ORGANISM: human
US-10-308-817-60

Query Match 100.0%; Score 28; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 31 DYGM 35

RESULT 12
US-10-032-037B-61
Sequence 61, Application US/10032037B
Publication No. US20040001822A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/44
CURRENT APPLICATION NUMBER: US/10/032.037B
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-037B-61

Query Match 100.0%; Score 28; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 31 DYGM 35

RESULT 13
US-10-029-988B-61
Sequence 61, Application US/10029988B
Publication No. US20040001839A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029.988B
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-029-988B-61

Query Match 100.0%; Score 28; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 31 DYGM 35

RESULT 14
US-10-032-423A-61
Sequence 61, Application US/10032423A
Publication No. US20040002450A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/45
CURRENT APPLICATION NUMBER: US/10/032.423A
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-423A-61

Query Match 100.0%; Score 28; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 31 DYGM 35

RESULT 15
US-10-453-698-60
Sequence 60, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
APPLICANT: Rocher, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453.698
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60
LENGTH: 98
TYPE: PRT
ORGANISM: human
US-10-453-698-60

Query Match 100.0%; Score 28; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 31 DYGM 35

Search completed: April 25, 2005, 21:09:48
Job time : 3.21175 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: April 25, 2005, 19:57:16 ; Search time 0.576497 Seconds
(Without alignments)
834.495 Million cell updates/sec

Title: US-10-029-926d-114

Perfect score: 28

Sequence: 1 DYGMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	98	2 S26928	Ig heavy chain V r
2	28	100.0	112	2 PH1654	Ig heavy chain V r
3	28	100.0	119	2 A43413	Ig heavy chain V r
4	28	100.0	227	2 AB1076	probable fibrin
5	28	100.0	268	2 H84684	En/Spm-like transp
6	28	100.0	268	2 T04660	hypothetical prote
7	28	100.0	334	2 H95307	arginine deiminase
8	28	100.0	340	2 H72681	hypothetical prote
9	28	100.0	411	2 S74760	hypothetical prote
10	28	100.0	448	2 AB3043	oxidoreductase Atu
11	28	100.0	468	2 B98233	hypothetical prote
12	28	100.0	474	2 T38737	probable CRAX pre
13	28	100.0	478	2 F89651	protein T04F8.2 (1
14	28	100.0	502	2 T24471	hypothetical prote
15	28	100.0	609	2 H71285	probable cell divi
16	28	100.0	650	2 G87572	calcium-binding pr
17	28	100.0	756	2 D96577	protein P27J15.24
18	28	100.0	830	2 I50455	prolactin receptor
19	28	100.0	869	2 A25945	coagulation factor
20	28	100.0	916	2 B84473	copii-like retroel
21	28	100.0	1008	2 H85055	probable transpos
22	28	100.0	1250	2 T27706	hypothetical prote
23	28	100.0	2133	2 T42763	coagulation factor
24	28	100.0	2319	2 A47004	coagulation factor
25	28	100.0	2351	1 EZHU	coagulation factor
26	28	89.3	109	2 T47696	hypothetical prote
27	28	89.3	113	2 B36259	Ig heavy chain V r
28	25	89.3	136	2 S35759	BHD9D10 protein -
29	25	89.3	138	1 D69979	conserved hypochet

30	25	89.3	145	2 D69383	conserved hypochet
31	25	89.3	154	2 B61027	hypothetical prote
32	25	89.3	171	2 S69895	helicase (EC 3.6.1
33	25	89.3	188	2 T48671	extracellular heme
34	25	89.3	203	2 T05519	hypothetical prote
35	25	89.3	203	2 C85288	hypothetical prote
36	25	89.3	220	2 H81048	biopolymer transp
37	25	89.3	233	1 F69178	conserved hypochet
38	25	89.3	238	2 H70734	hypothetical prote
39	25	89.3	250	2 C85040	hypothetical prote
40	25	89.3	251	2 D69861	RNA polymerase sig
41	25	89.3	264	2 AF3550	phosphoglycolate p
42	25	89.3	277	2 S76396	hypothetical prote
43	25	89.3	289	2 AI3166	hypothetical prote
44	25	89.3	291	2 A69545	mRNA 3'-end proces
45	25	89.3	298	2 T29685	hypothetical prote

ALIGNMENTS

RESULT 1

S26928
Ig heavy chain V region (DP-32) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26928
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; WUID:93021117; PMID:1404388
A:Accession: S26928
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12334; NID:G32887; PID:CAA78204.1; PID:G32888
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||||
Db 31 DYGMS 35

RESULT 2

PH1654
Ig heavy chain V region (clone 6H9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1654
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saseo, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphyl.
A:Reference number: PH1642; WUID:93301610; PMID:8315388
A:Accession: PH1654
A:Molecule type: mRNA
A:Residues: 1-112 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYGMS 5
|||||

Db 23 DYGMS 27

RESULT 3

A43413

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C/Accession: A43413

R/Tomiyama, Y.; Brojer, E.; Rugelei, Z.M.; Shattil, S.J.; Smiltnick, J.; Gorski, J.; Kum

J. Biol. Chem. 267, 18085-18097, 1992

A/Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific

A/Reference number: A43413; MUID:21368177; PMID:1517241

A/Accession: A43413

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-119 <TOM>

A/Note: sequence extracted from NCBI backbone (NCBIP:112815)

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:9-92/Domain: immunoglobulin homology <IM>

Query Match

100.0%; Score 28; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

|||||

Db 25 DYGMS 29

RESULT 4

AB1076

probable fimbrial chaperone protein ehbA [imported] - Salmonella enterica subsp. enteric

C/Species: Salmonella enterica subsp. enterica serovar Typh

A/Note: this species has also been called Salmonella typh

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AB1076

R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moutle, S.; O'Garra, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:1167608

A/Accession: AB1076

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-227 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD03425.1; PID:G16505691; GSPDB:GN00176

C/Genetics:

A/Gene: ehbA

C/Superfamily: chaperone protein papD

Query Match

100.0%; Score 28; DB 2; Length 227;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

|||||

Db 215 DYGMS 219

RESULT 5

H84684

En/Spm-like transposon protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: H84684

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;

Euseb, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: AB4420; MUID:20083487; PMID:10617197

A/Accession: H84684

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-268 <STO>

A/Cross-references: UNIPROT:Q9SKM6; GB:AE002093; NID:G4432833; PIDN:AAD20682.1; GSPDB:G

A/Gene: AC2928440

A/Map position: 2

Query Match

100.0%; Score 28; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

|||||

Db 218 DYGMS 222

RESULT 6

T04660

hypothetical protein F8D20_60 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T04660

R/Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes

submitted to the Protein Sequence Database, July 1998

A/Reference number: Z15381

A/Accession: T04660

A/Molecule type: DNA

A/Residues: 1-268 <BEV>

A/Cross-references: UNIPROT:O81788; EMBL:AL031135

A/Experimental source: cultivar Columbia; BAC clone F8D20

C/Genetics:

A/Map position: 4

A/Intons: 75/1; 241/1

A/Note: F8D20_60

Query Match

100.0%; Score 28; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

|||||

Db 263 DYGMS 267

RESULT 7

H95307

arginine deiminase (EC 3.5.3.6) ArCB [imported] - Sinorhizobium meliloti (strain 1021)

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C/Accession: H95307

R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow

A/Authors: Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001

A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo-

A/Reference number: A95262; MUID:21396509; PMID:11481432

A/Accession: H95307

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-334 <KUR>

A/Experimental source: UNIPROT:Q9Z2T1; GB:AE006469; PIDN:AAK65026.1; PID:G14523456; GSPDB:G

R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

pell, D.; Chaim, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

hebut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation
 C:Genetics:
 A:Gene: arcb
 A:Genome: plasmid
 C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
 C:Keywords: hydrolase

Query Match 100.0%; Score 28; DB 2; Length 334;
 Best Local Similarity 100.0%; Pred. No. 73;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
 |||||
 Db 292 DYGMS 296

RESULT 8
 H72681
 hypothetical protein APE0874 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: H72681
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A:Reference number: A72450; PMID:9310339; PMID:10382966

A:Accession: H72681
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-340 <KAM>
 A:Cross-references: UNIPROT:Q9YDPI; DDBJ:AP000060; NID:G5104188; PIDD:BA79856.1; PIDD:G5104188

A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0874

C:Superfamily: Aeropyrum pernix hypothetical protein APE0874

Query Match 100.0%; Score 28; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 75;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
 |||||
 Db 82 DYGMS 86

RESULT 9

S74760
 hypothetical protein slr1617 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S74760
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1995

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC 6803
 A:Reference number: S74322; PMID:97061201; PMID:8905231

A:Accession: S74760
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-411 <KAN>
 A:Cross-references: UNIPROT:P72895; EMBL:D90901; GB:AB001339; NID:G1651897; PIDD:BA1691

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 100.0%; Score 28; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
 |||||
 Db 65 DYGMS 69

RESULT 10

AB3043
 oxidoreductase Atu3958 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AB3043
 R:Wood, D.W.; Seubald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Moo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; Mclellan, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:121608550; PMID:11743193

A:Accession: AB3043
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-448 <KUR>
 A:Cross-references: UNIPROT:Q8U8Y0; GB:AE008689; PIDD:AAU4760.1; PIDD:G17742396; GSPDB:1G7742396

A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu3958

A:Map position: linear chromosome

Query Match 100.0%; Score 28; DB 2; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
 |||||
 Db 124 DYGMS 128

RESULT 11
 B98243
 hypothetical protein AGR L 1791 [imported] - Agrobacterium tumefaciens (strain C58, Cer

C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: B98243
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.

Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58

A:Reference number: A97359; PMID:121608551; PMID:11743194
 A:Accession: B98243

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-468 <KUR>
 A:Cross-references: UNIPROT:Q8U8Y0; GB:AE007870; PIDD:AAK89468.1; PIDD:G15159336; GSPDB:1G15159336

A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: AGR L 1791

A:Map position: linear chromosome

Query Match 100.0%; Score 28; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 11e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
 |||||
 Db 144 DYGMS 148

RESULT 12
 T38737
 probable CAXX prenyl proteinase 1 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T38737
 R:Gentles, S.; Churcher, C.M.; Bartell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, December 1995
 A:Reference number: Z21808

A:Accession: T38737

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-448 <KUR>
 A:Cross-references: UNIPROT:Q8U8Y0; GB:AE007870; PIDD:AAK89468.1; PIDD:G15159336; GSPDB:1G15159336

A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: AGR L 1791

A:Map position: linear chromosome

A/Accession: T38737
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-474 <GEN>
 A/Cross-references: UNIPROT:Q10071; EMBL:Z68144; PIDN:CAA92258.1; GSPDB:GN00066; SPDB:SF
 A/Experimental source: strain 97zh-; cosmid c3H1
 C/Genetics:
 A/Gene: SPDB:SPAC3H1.05
 A/Map position: 1
 A/Introns: 35/3

Query Match 100.0%; Score 28; DB 2; Length 474;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 Db 349 DYGMS 353

RESULT 13

F89651
 Protein T04F8.2 [imported] - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: F89651
 R/Anonymous: The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A/Reference number: A75000; MID:99069613; PMID:9851916
 A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
 A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A/Accession: F89651
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-478 <STO>
 A/Cross-references: UNIPROT:Q22162; GB:chr X; PIDN:CAA91478.1; PID:G3924836; GSPDB:GN000
 C/Genetics:
 A/Gene: T04F8.2
 A/Map position: X
 C/Superfamily: Caenorhabditis elegans hypothetical protein T04F8.2

Query Match 100.0%; Score 28; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 Db 77 DYGMS 81

RESULT 14

T24471
 hypothetical protein T04F8.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T24471
 R/Lennard, N.
 submitted to the EMBL Data Library, November 1995
 A/Reference number: Z19895
 A/Accession: T24471
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-502 <WTL>
 A/Cross-references: UNIPROT:Q22162; EMBL:Z66565; PIDN:CAA91478.2; GSPDB:GN00028; CESP:TC
 A/Experimental source: clone T04F8
 C/Genetics:
 A/Gene: CESP:T04F8.2
 A/Map position: X
 A/Introns: 26/1; 72/1; 103/3; 162/2; 214/3; 249/2; 290/2; 340/3; 382/2; 427/1; 459/2
 C/Superfamily: Caenorhabditis elegans hypothetical protein T04F8.2

Query Match 100.0%; Score 28; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 Db 93 DYGMS 97

RESULT 15

H71285
 probable cell division protein (ftsH) - syphilis spirochete
 C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C/Accession: H71285
 R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
 reon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mcb
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A/Reference number: A71250; MID:98332770; PMID:965876
 A/Accession: H71285
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-609 <COL>
 A/Cross-references: UNIPROT:O83746; GB:AE001247; GB:AE000520; MID:G3323059; PIDN:AAC657
 A/Experimental source: strain Nichols
 C/Genetics:
 A/Gene: TP0765
 C/Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain hom
 F/155-363/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>

Query Match 100.0%; Score 28; DB 2; Length 609;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 Db 493 DYGMS 497

Search completed: April 25, 2005, 20:24:10
 Job time : 2.5765 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 2.58315 Seconds
(without alignments)
991.192 Million cell updates/sec

Title:	US-10-029-926D-114
Perfect score:	28
Sequence:	1 DYGMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      1612378 segs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	100.0	70	2	084Z47	084Z47 Oryza sativa
2	28	100.0	112	2	09HCC1	09HCC1 homo sapiens
3	28	100.0	195	2	0726K5	0726K5 desulfivibrio
4	28	100.0	204	2	0088Z3	0088Z3 mus musculus
5	28	100.0	204	2	0088Z6	0088Z6 mus musculus
6	28	100.0	206	2	069X89	069X89 Oryza sativa
7	28	100.0	227	2	08Z0S8	08Z0S8 salmonella
8	28	100.0	227	2	08ZUT0	08ZUT0 salmonella
9	28	100.0	242	2	06GR19	06GR19 xenopus laevis
10	28	100.0	245	2	06E260	06E260 arabidopsis
11	28	100.0	246	2	06NU71	06NU71 xenopus laevis
12	28	100.0	249	2	08E110	08E110 streptococcus
13	28	100.0	255	2	06GMS0	06GMS0 xenopus laevis
14	28	100.0	268	2	08I788	08I788 arabidopsis
15	28	100.0	268	2	09SKM6	09SKM6 arabidopsis
16	28	100.0	280	2	0742X5	0742X5 mycobacterium
17	28	100.0	293	2	08PFN0	08PFN0 xanthomonas
18	28	100.0	300	2	09C840	09C840 arabidopsis
19	28	100.0	302	2	09M7X8	09M7X8 arabidopsis
20	28	100.0	333	2	06L162	06L162 picophyllus
21	28	100.0	334	1	OTCC_RHIME	09ZCZ1 ribichium m
22	28	100.0	340	2	09YDP1	09YDP1 aeropyrum p
23	28	100.0	352	1	06T411	06T411 sus scrofa
24	28	100.0	354	1	CKR5_MOUSE	P51682 mus musculus
25	28	100.0	361	2	07CCP5	07CCP5 escherichia
26	28	100.0	362	2	09ITC3	09ITC3 arabidopsis
27	28	100.0	406	2	09EY89	09EY89 rhicobium s
28	28	100.0	411	2	P72895	P72895 synchococcus
29	28	100.0	439	2	08RT65	08RT65 vibrio parva
30	28	100.0	448	2	08U8Y0	08U8Y0 agrobacterium
31	28	100.0	448	2	0880T6	0880T6 pseudomonas

32	28	100.0	468	2	OTCTO2	OTCTO2	agrobacteri
33	28	100.0	474	1	ST74_SCHPO	Q10071	schizosacch
34	28	100.0	486	2	Q8L4E4	Q8L4E4	oryza sativ
35	28	100.0	493	1	OCULN_XENNA	Q9JN01	xenopus lae
36	28	100.0	502	2	Q22162	Q22162	caenorhabdi
37	28	100.0	517	2	Q6CCU2	Q6CCU2	yarrowia 11
38	28	100.0	519	2	Q6C048	Q6C048	xenopus lae
39	28	100.0	532	2	Q7XR43	Q7XR43	oryza sativ
40	28	100.0	537	2	Q91F86	Q91F86	chilo iride
41	28	100.0	560	2	Q6FEU4	Q6FEU4	acinetobact
42	28	100.0	572	2	P87247	P87247	botrytis ci
43	28	100.0	572	2	Q98AA9	Q98AA9	thiosulfium
44	28	100.0	603	2	Q8S9H3	Q8S9H3	clostridium
45	28	100.0	609	1	FTSH_TREPA	Q83746	treponema p

ALIGNMENTS

RESULT 1
084Z47 PRELIMINARY; PRT; 70 AA.
ID Q84Z47
AC Q84Z47;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0456G06.105 (Hypothetical protein OSUBA0039C01.1142).
GN Name=P0456G06.105; Synonyms=OSUBA0039C01.1142;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartidae; Oryzeae; Oryza.
OK NCBI_taxonomy=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0456G06.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. [2]
RN RN
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC clone:OSUBA0039C01.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; AP005051; BACS7333.1; -.
DR EMBL; AP005768; BAD31689.1; -. DR Gramene; O84Z47; -.
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7281 MW; FE752CC92EB2B85 CRC64;
Query Match 100.0%; Score 28; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DYGSMS 5 Db 34 DYGSMS 38
RESULT 2
09HCCL PRELIMINARY; PRT; 112 AA.
ID 09HCCL
AC 09HCCL;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment). OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OK NCBI_taxonomy=9606;

```

RN (1)
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB049915; BAB16829.1; -.
DR HSSP: P01783; 11GC.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003596; IG_V.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 112;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 31 DYGSMS 35

RESULT 3
ID Q726K5 PRELIMINARY; PRT; 195 AA.
AC Q726K5;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OederedocguNames=DVU3102;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heideberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., Deboy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uetzelback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL: AB017319; AAS97573.1; -.
DR TIGR: DVU3102; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0008565; F:protein transporter activity; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR InterPro: IPR006260; TonB_C.
DR TIGRfams: TIGR01352; TonB_Cterm; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 195 AA; 19904 MW; DF156A576C05C412 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 195;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 82 DYGSMS 86

RESULT 4
ID O08823 PRELIMINARY; PRT; 204 AA.

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AC O08823;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Axonemal dynein heavy chain (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=NRRI; TISSUE=Testis;
RC MEDLINE=98038992; PubMed=9373155; DOI=10.1016/S0378-1119(97)00417-4;
RA Neesen J., Koehle M., Kirschne R., Steinlein C., Kreutzberger J.,
RA Engel W., Schmid M.;
RT "Identification of dynein heavy chain genes expressed in human and
RT mouse testis: chromosomal localization of an axonemal dynein gene."
RL Gene 200:193-202(1997).
DR EMBL: Z83810; CAB06064.1; -.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22198 MW; 72756AAB52D0B84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 204;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 199 DYGSMS 203

RESULT 5
ID O08826 PRELIMINARY; PRT; 204 AA.
AC O08826;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Axonemal dynein heavy chain (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=NRRI; TISSUE=Testis;
RC MEDLINE=98038992; PubMed=9373155; DOI=10.1016/S0378-1119(97)00417-4;
RA Neesen J., Koehle M., Kirschne R., Steinlein C., Kreutzberger J.,
RA Engel W., Schmid M.;
RT "Identification of dynein heavy chain genes expressed in human and
RT mouse testis: chromosomal localization of an axonemal dynein gene."
RL Gene 200:193-202(1997).
DR EMBL: Z83813; CAB06067.1; -.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22449 MW; 9AFDA82E4603746 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 204;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 199 DYGSMS 203

RESULT 6
ID O69K89 PRELIMINARY; PRT; 206 AA.
AC O69K89;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)

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DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Hypochemical protein OSJNB0079K1.23.
 GN Name=OSJNB0079K1.23;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 NC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasakura T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
 clone:OSJNB0079K1.1";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP005971; BAD36615.1; -
 KM Hypochemical protein
 SQ SEQUENCE 206 AA; 23255 MW; 9628AC2F986F43D2 CRC64;
 SO
 Query Match 100.0%; Score 28; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGM 5
 DB 120 DYGM 124
 RESULT 7
 Q8Z0S8 PRELIMINARY; PRT; 227 AA.
 AC Q8Z0S8; Q7C4S5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Putative fimbrial chaperone protein.
 GN Name=ctb; OrderedLocNames=STY4943, t4633;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 NC NCB1_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng M., Liu S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the periplasmic pilus chaperone family.
 DR EMBL: AL627284; CAP03425.1; -
 DR EMBL: AB016849; AA072062.1; -
 DR HSP; P28926; 1P5U.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0007047; P:cell wall organization and biogenesis; IEA.

DR GO; GO:0006457; P:protein folding; IEA.
 DR Pfam; PF02753; Pili_assembly_N; 1.
 DR Pfam; PF00345; Pili_assembly_C; 1.
 DR PRINTS: PR00969; CHAPERONPili.
 DR ProDom; PD001447; Pili_chaperone; 1.
 DR PROSITE; PS00635; Pili_CHAPERONE; 1.
 KM Chaperone; Complete proteome.
 SQ SEQUENCE 227 AA; 24829 MW; 6E8F92D7B5421AD1 CRC64;
 SO
 Query Match 100.0%; Score 28; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGM 5
 DB 215 DYGM 219
 RESULT 8
 Q8ZU0 PRELIMINARY; PRT; 227 AA.
 AC Q8ZU0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 26, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Putative fimbrial chaperone protein.
 GN Name=ctb; OrderedLocNames=STM4594;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 NC NCB1_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RX McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2";
 RL Nature 413:852-856(2001).
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the periplasmic pilus chaperone family.
 DR EMBL: AB008916; ALA23409.1; -
 DR HSP; P28926; 1P5U.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0007047; P:cell wall organization and biogenesis; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR Pfam; PF02753; Pili_assembly_C; 1.
 DR Pfam; PF00345; Pili_assembly_N; 1.
 DR PRINTS: PR00969; CHAPERONPili.
 DR ProDom; PD001447; Pili_chaperone; 1.
 DR PROSITE; PS00635; Pili_CHAPERONE; 1.
 KM Chaperone; Complete proteome.
 SQ SEQUENCE 227 AA; 24743 MW; EC0D30D9487CD7DF CRC64;
 SO
 Query Match 100.0%; Score 28; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGM 5
 DB 215 DYGM 219
 RESULT 9
 Q6GR19 PRELIMINARY; PRT; 242 AA.
 AC Q6GR19;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE MGCB1350 protein.
GN Name=MGCB1350;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Gerhard D.S.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071115; AAH7115.1; -
SQ SEQUENCE 242 AA; 27476 MW; 203357C8C1AE809 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. NO.3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYCGMS 5
| | | | |
Db 35 DYCGMS 39

RESULT 10
Q6E260 PRELIMINARY; PRT; 245 AA.
ID O6E260;
AC O6E260;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 23-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE Hypochemical protein.
GN ORFNames=At3G06710;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;

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RN [1]
RP SEQUENCE FROM N.A.
RA Xiao Y., Underwood B., Moskal W., Torian U., Redman J., Wu H.C.,
RA Utecherback T., Town C.D.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; At600563; AA168362.1; -
KW Hypochemical protein.
SQ SEQUENCE 245 AA; 27802 MW; 43C5412313106AB CRC64;

Query Match 100.0%; Score 28; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. NO.3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYCGMS 5
| | | | |
Db 40 DYCGMS 44

RESULT 11
Q6N711 PRELIMINARY; PRT; 246 AA.
ID O6N711;
AC O6N711;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE MGCB1187 protein.
GN Name=MGCB1187;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX Klein S., Strausberg R.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068729; AAH68729.1; -
DR InterPro; IPR000504; RNA_rec_mot.
PFam; PF00076; RRM_1; 1.

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DR SMART; SM00360; RM; 1.
DR PROSITE; PSS0102; RM; 1.
SQ SEQUENCE 246 AA; 27984 MW; 59F317B368FD6825 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 246;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
DB 111 DYGM5 115

RESULT 12
OGBE110 PRELIMINARY; PRT; 249 AA.
ID OGBE110
AC OGBE110;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Prophage lambdaSal, antirepressor, putative.
GN OrderedLocustNames=SAG0555;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=1200547; DOI=10.1073/pnas.182380799;
RA Tetselin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Khouli H.M., Mulligan S.,
RA Garry H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL EMBL; AEO14217; AAM99456.1; -.
DR TIGR; SAG0555; -.
KW Complete proteome.
SQ SEQUENCE 249 AA; 29176 MW; F6537740D2C89258 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 249;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
DB 163 DYGM5 167

RESULT 13
OGBM50 PRELIMINARY; PRT; 255 AA.
ID OGBM50
AC OGBM50;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE MGC83967 protein.
GN Name=MGC83967;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.T., Wang J., Helin P.,
RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Prange C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Straube R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391(2002).

[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074235; AAT74235.1; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PR00076; RM1.1; 1.
DR SMART; SM00360; RM; 1.
DR PROSITE; PSS0102; RM; 1.
SQ SEQUENCE 255 AA; 29100 MW; 16D60838A5FD8D85 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 255;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
DB 111 DYGM5 115

RESULT 14
OBI788 PRELIMINARY; PRT; 268 AA.
ID OBI788
AC OBI788;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Homodomain - like protein (AT4935550/F8D20_60) (WOX13 protein).
GN Name=F8D20_60; Synonyms=AT4935550;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Koester P., Hempel S., Entian K.-D., Hohenseil J., Jesse T.,
RA Heijnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

[2]
RP SEQUENCE FROM N.A.
RC EU Arabidopsis sequencing project;

```

```

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh U., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA Kamitani A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shim P., Bowser L., Carninci P.,
RA Chan W.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan W.W., Ishida J., Jones T., Kamitani A., Karlin-Neumann G.,
RA Nguyen J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Haecker A., Gross-Hardt R., Geiges B., Sarkar A., Breuninger H.,
RA Herrmann M., Laux T.;
RT "Expression dynamics of WOX genes mark cell fate decisions during
RT early embryonic patterning in Arabidopsis thaliana.";
RL Development 0:0-0(2004).
RN [6]
RP SEQUENCE FROM N.A.
RA Roe M., Hempel S., Entian K.-D., Meves H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
DR EMBL, AL031135; CA20025.1; -
DR EMBL, AY048268; AAK82530.1; -
DR EMBL, BT000538; AANI8107.1; -
DR EMBL, AY251404; AAP37142.1; -
DR EMBL, AL161587; CAB80271.1; -
DR PIR, T04660; T04660.
DR GO, GO:0005634; C:nucleus; IEA.
DR GO, GO:0003700; F:transcription factor activity; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR013156; Homeobox.
DR InterPro, IPR009057; Homeobox_like.
DR Pfam, PF00046; Homeobox; 1.
DR ProDom, PD000010; Homeobox; 1.
DR SMART, SM00389; HOX; 1.
DR PROSITE, PS00071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ
SEQUENCE 268 AA; 29673 MW; D57FCC13AB1A93DA CRC64;

Query Match 100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 263 DYGM 267

RESULT 15
ID Q9SKM6 PRELIMINARY; PRT; 268 AA.
AC Q9SKM6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

```

```

DE En/Spm-like transposon protein.
GN Name=At2g28440;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Renning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC006283; AAD20682.1; -.
DR PIR; H84684; H84684.
SQ SEQUENCE 268 AA; 27741 MW; 0584FDE4622FE0E CRC64;

Query Match 100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. NO. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 DYGWS 5
DB 218 DYGWS 222

Search completed: April 25, 2005, 20:34:02
Job time : 4.58315 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 10.4224 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926D-115
Perfect score: 96
Sequence: 1 GINWNGSTGYADSVKX 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	17	3 AAY95192	Aay95192 Anti-Plat
2	96	100.0	17	5 ABG78240	Abg78240 Human Fv
3	96	100.0	17	5 ABG91931	Abg91931 Human ant
4	96	100.0	98	3 AAB40073	Aab40073 Anti-H1L1
5	96	100.0	98	5 ABG78186	Abg78186 Human Fv
6	96	100.0	98	5 ABG91877	Abg91877 Human ant
7	96	100.0	98	6 ABO27087	Aboc27087 Human ger
8	96	100.0	98	7 ADF09916	Adf09916 Antibody
9	96	100.0	98	7 ADF10126	Adf10126 Antibody
10	96	100.0	98	7 ADF10024	Adf10024 VEGF anti
11	96	100.0	98	7 ADJ80300	Adj80300 VH gene 1
12	96	100.0	113	3 AAY95177	Aay95177 Anti-Plat
13	96	100.0	113	3 AAY95178	Aay95178 Anti-Plat
14	96	100.0	115	3 AAY95189	Aay95189 Anti-Plat
15	96	100.0	115	3 AAY95190	Aay95190 Anti-Plat
16	96	100.0	116	2 AAW19880	Aaw19880 CEA-speci
17	96	100.0	117	2 AAR66312	Aar66312 Human imm
18	96	100.0	118	4 AAU02560	Aau02560 Anti-adip
19	96	100.0	122	3 AAY96065	Aay96065 Human ant
20	96	100.0	123	8 ADJ57861	Adj57861 Light var
21	96	100.0	207	5 AAU98019	Aau98019 Human ace
22	96	100.0	207	5 ADR28086	Adr28086 NFB polyp
23	96	100.0	238	8 AAY95198	Aay95198 Anti-Plat
24	96	100.0	239	5 ABP46004	Abp46004 Human Bly
25	96	100.0	239	5 ABP46027	Abp46027 Human Bly

26	96	100.0	239	5 ABP44926	Abp44926 Human Bly
27	96	100.0	239	7 ADG35753	Adg35753 Single ch
28	96	100.0	239	7 ADG36854	Adg36854 Single ch
29	96	100.0	239	7 ADG36831	Adg36831 Single ch
30	96	100.0	242	7 ADG30497	Adg30497 Human GMC
31	96	100.0	242	8 ADI58068	Adi58068 Reg IV-ep
32	96	100.0	244	6 AAO31136	Aao31136 Human CM0
33	96	100.0	246	5 ABG78329	Abg78329 Human Fv
34	96	100.0	246	5 ABG92026	Abg92026 Antibody
35	96	100.0	249	7 ADG30407	Adg30407 Human GMB
36	96	100.0	256	5 ABG78334	Abg78334 Human Fv
37	96	100.0	256	5 ABG92025	Abg92025 Antibody
38	96	100.0	266	5 ABG92020	Abg92020 Human ant
39	96	100.0	277	5 ABG78150	Abg78150 Human Fv
40	96	100.0	277	5 ABG78328	Abg78328 Human Fv
41	96	100.0	277	5 ABG92019	Abg92019 Human ant
42	96	100.0	277	5 ABG91841	Abg91841 Human ant
43	96	100.0	277	8 ADI28366	Adi28366 Human scf
44	96	100.0	278	8 ADI28367	Adi28367 Human scf
45	96	100.0	280	8 ADI28368	Adi28368 Human scf

ALIGNMENTS

RESULT 1	
ID AAY95192	standard; peptide; 17 AA.
AC AAY95192;	
DT 29-AUG-2000	(first entry)
DE Anti-platelet glycoprotein Ib human H1b-1 VH CDR2.	
XX	
KM Variable heavy chain; single chain antibody; scFv; human; H1b-1;	
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;	
KM antithrombotic; thrombus; therapy; diagnostic; CDR2;	
KW complementarity determining region.	
XX	
OS Homo sapiens.	
XX	
PN WO200026667-A1.	
XX	
PD 11-MAY-2000.	
XX	
PF 29-OCT-1999;	99WO-US025495.
XX	
PR 30-OCT-1998;	98US-0106275P.
XX	
PA (MILL.) MILLER J L.	
XX	
PI Miller JL;	
XX	
DR WPI; 2000-365744/31.	
XX	
PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein	
PT Ib alpha molecule useful for producing antibodies which inhibit platelet	
PT aggregation.	
XX	
PS Claim 15; Fig 5; 89pp; English.	
XX	
CC The present sequence is that of complementarity determining region 2	
CC (CDR2) of the heavy chain variable region (VH) of human single chain	
CC antibody (scFv) H1b-1 (see AAY95198), which is directed against platelet	
CC glycoprotein Ib (GP1b). The H1b series of scFv was isolated from a human	
CC synthetic VH and VL scFv library on the basis of their binding to	
CC platelet GP1b. Whether displayed as surface proteins on a phagemid or	
CC secreted as free scFv by Escherichia coli, the H1b scFv clones are	
CC capable of inhibiting von Willebrand factor-dependent aggregation of	
CC platelets. The scFv are composed of native human protein sequences and	
CC are therefore attractive potential reagents for therapeutic purposes.	
CC They provide a new class of antithrombotic agents, useful for the	

CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIIb/IIIa receptor, of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL
 CC chain, including CDR fragments, are also claimed

XX Sequence 17 AA;

Query Match 100.0%; Score 96; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 17
 1 GINWNGSGTGYADSVK 17

Db 1 GINWNGSGTGYADSVK 17

RESULT 2

ABG78240 ID ABG78240 standard; peptide; 17 AA.

XX AC ABG78240;

DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #115.

XX KM Human: Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;

XX KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plakain D, Peretz T;

XX XX WPI; 2002-619166/66.

XX DR Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

XX PS Claim 20; Page 208-209; 232pp; English.

XX CC The invention relates to a peptide or polypeptide comprising an Fv

XX CC molecule, a construct or fragments or a construct of a fragment with

XX CC enhanced binding characteristics which selectively and/or specifically

XX CC binds to a target cell in favour of other cells, where binding is

XX CC primarily determined by a first hypervariable region and Fv is a single

XX CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX CC association with or attached, coupled, combined, linked or fused to a

XX CC pharmaceutical agent, is useful in the manufacture of a medicament, where

XX CC the medicament has activity against a diseased cell, preferably a cancer

XX CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,

XX CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an

XX CC acute myeloid leukemia cell). The peptide is also useful for preparing a

XX CC composition for use in inhibiting the growth of a diseased or cancer

XX CC cell. This sequence represents a human Fv molecule hypervariable region

XX CC related peptide of the invention

XX XX Sequence 17 AA;

Query Match 100.0%; Score 96; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 17
 1 GINWNGSGTGYADSVK 17

Db 1 GINWNGSGTGYADSVK 17

RESULT 3

ABG91931 ID ABG91931 standard; peptide; 17 AA.

XX AC ABG91931;

DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #115.

XX KM Human: antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX KM metastasis; hypervariable region; autoimmune disease; thrombosis;

XX KM restenosis; leukemia; inflammatory disease; cardiovascular disease;

XX KM myocardial infarction; retinopathic disease; abnormal platelet function;

XX KM sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;

XX PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX XX WPI; 2002-674776/72.

XX DR Novel isolated epitope present on cancer cells and important in

XX PT physiological phenomena such as cell rolling, metastasis and

XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular

XX PT diseases, and cancer.

XX PS Claim 25; Page 284-285; 0pp; English.

XX CC The invention relates to an isolated epitope present on cancer cells and

XX CC important in physiological phenomena such as cell rolling, metastasis and

XX CC inflammation, where the epitope is capable of being bound by an antibody,

XX CC its antigen-binding fragment or its complex comprising at least one

XX CC antibody or its binding fragment having a first hypervariable region. The

XX CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

XX CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

XX CC tumour or leukemia cells, increase in number of tumour or leukemia

XX CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

XX CC platelet and/or cell-platelet adhesion or aggregation, for increasing

XX CC mortality of tumour or leukemia cells, for increasing the susceptibility

XX CC of diseased cells to damage by anti-disease, anti-cancer or anti-

XX CC leukemia agents, or for decreasing the number of tumour or leukemia

XX CC cells in a patient, or in the manufacture of a medicament for the above

XX CC mentioned purposes. The epitopes are useful for diagnosing and treating

XX CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory

XX CC diseases, cardiovascular diseases such as myocardial infarction,

XX CC retinopathic diseases and other diseases mediated by abnormal platelet

XX CC function and diseases caused by sulphated tyrosine-dependent protein-

XX CC protein interactions. This sequence represents a human antibody fragment

XX CC of the invention

XX XX

SQ Sequence 17 AA;
Query Match 100.0%; Score 96; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGYADSVKG 17
1 GINWNGSGTGYADSVKG 17
DB 1 GINWNGSGTGYADSVKG 17

RESULT 4
AAB40073
ID AAB40073 standard; protein; 98 AA.
XX AAB40073;
AC AAB40073;
DT 05-FEB-2001 (first entry)
XX
XX
DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 599.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antileukemic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
XX Homo sapiens.
OS
XX
XX WO200056772-A1.
PN
XX
XX 28-SEP-2000.
PD
XX
XX 24-MAR-2000; 2000WO-US007946.
PF
XX
XX 25-MAR-1999; 99US-0126603P.
PR
XX
XX (BADI) BASF AG.
PA (GEMV) GENETICS INST INC.
XX
XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Valdman GM, Venturini A, Warne NW, Widom A, Bivlin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
XX WPI; 2000-638250/61.
DR
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis.
PS
XX Claim 75; Page 121; 377pp; English.
XX
XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAC61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antirheumatic; antiarthritic; antileukemic; antiasthmatic; cardiant;
CC neuroprotective; antipsoriatic; antiparasitic; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders

XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 96; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGYADSVKG 17
1 GINWNGSGTGYADSVKG 17
DB 50 GINWNGSGTGYADSVKG 66

RESULT 5
ABG78186
ID ABG78186 standard; protein; 98 AA.
XX ABG78186;
AC ABG78186;
DT 15-NOV-2002 (first entry)
XX
XX
DE Human Fv molecule hypervariable region related peptide #61.
XX
XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200259264-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 31-DEC-2001; 2001WO-US049440.
PF
XX
XX 29-DEC-2000; 2000US-00751181.
PR
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
PA
XX
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
PI Plakstin D, Peretz T;
XX WPI; 2002-619166/66.
DR
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
PS
XX Claim 13; Page 177-178; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has actively against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 96; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGYADSVKG 17

Db 50 GINMNGSGTGYADSVKG 66

RESULT 6

ABG91877
ID ABG91877 standard; protein; 98 AA.

XX ABG91877;
XX

DT 04-DEC-2002 (first entry)
XX

DE Human antibody fragment #61.
XX

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX metastasis; hypervariable region; autoimmune disease; thrombosis;
XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX myocardial infarction; retinopathic disease; abnormal platelet function;
XX sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.
XX

PN W0200253700-A2.
XX

PD 11-JUL-2002.
XX

PF 31-DEC-2001; 2001WO-US049442.
XX

PR 29-DEC-2000; 2000US-00751181.
XX

PR 29-DEC-2000; 2000US-0258948P.
XX

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX

PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Sanchon B, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

DR WPI; 2002-674776/72.
XX

PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.

XX
XX
XX Disclosure; Page 255; Ovp; English.

CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
CC
CC
XX

XX Sequence 98 AA;
SQ

Query Match 100.0%; Score 96; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINMNGSGTGYADSVKG 17
Db 50 GINMNGSGTGYADSVKG 66

RESULT 7

ABO27087
ID ABO27087 standard; protein; 98 AA.

XX ABO27087;
XX

DT 10-SEP-2003 (first entry)
XX

DE Human germline heavy chain variable region gene segment #20.
XX

XX Human; heavy chain variable region; VH; humanised antibody;
XX chimeric antibody; complementarily determining region; CDR;
XX canonical CDR structure type.

XX Homo sapiens.
XX

PN US2003039649-A1.
XX

PD 27-FEB-2003.
XX

PF 12-JUL-2002; 2002US-00194975.
XX

PR 12-JUL-2001; 2001US-0305111P.
XX

PA (FOOTE) FOOTE J.
XX

PI Foote J;
XX

DR WPI; 2003-492151/46.
XX

PT Making humanized antibody for converting antibody, by making chimeric
PT antibodies containing complementarily determining region from non-human
PT antibody and appropriate framework sequences of human antibodies.

XX
XX
XX Example 1; Fig 1; 31pp; English.

CC The invention describes a method of making a humanised antibody,
CC comprising making chimeric antibodies containing a complementarily
CC determining region (CDR) from a non-human antibody and appropriate
CC framework sequences (I) of human antibodies. (I) is selected by using
CC canonical CDR structure types of non-human antibody in comparison to
CC germline canonical CDR structure types of human antibodies as the basis
CC for selection, for humanisation. The method is useful for making a
CC humanised antibody or a converted antibody. The method is applicable for
CC converting a subject antibody sequence of any subject species to a less
CC immunogenic form suitable for use in an object species. The method is
CC reliable for identifying suitable human framework sequences to support
CC non-human CDR regions and to provide humanised antibodies that retain
CC high antigen binding with low immunogenicity in humans, without the need
CC for direct comparison of framework sequences, without the need for
CC determining critically important amino acid residues in the framework,
CC and without the need for multiple iteration and construction to obtain
CC humanised antibodies with suitable therapeutic properties. The antibody
CC has high affinity and low immunogenicity without need for comparing
CC framework sequences between non-human and human antibodies. This sequence
CC represents a human heavy chain variable region gene segment used in the
CC creation of humanised antibodies
CC
CC
XX

XX Sequence 98 AA;
SQ

Query Match 100.0%; Score 96; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINMNGSGTGYADSVKG 17
Db 50 GINMNGSGTGYADSVKG 66


```

RESULT 8
ID ADF09916 standard; protein; 98 AA.
XX
XX ADF09916;
XX
XX 12-FEB-2004 (first entry)
XX
DE Antibody heavy chain variable region VH_3-20.
XX
XX Antibody; stability; solubility; antigen binding affinity;
XX variable region; human.
XX
XX Homo sapiens.
XX
XX WO2003074679-A2.
XX
XX 12-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-US006598.
XX
XX 01-MAR-2002; 2002US-0360843P.
XX
XX 29-MAY-2002; 2002US-0384197P.
XX
XX (XENC-) XENCOR.
XX
XX Lazar GA, Desjarlais JR, Marshall SA, Dahyat B;
XX
XX WPI; 2003-722066/68.
XX
XX Computer optimization of physicochemical properties of antibodies
XX comprises analyzing the interactions of amino acids at variable
XX positions.
XX
XX Disclosure; Fig 2a; 135pp; English.
XX
XX The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
XX
SQ Sequence 98 AA;
XX
Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GINWNGSGTGYADSVKG 17
DB 50 GINWNGSGTGYADSVKG 66
XX
RESULT 9
ADP10126
ID ADF10126 standard; protein; 98 AA.
XX
XX ADF10126;
XX
XX 12-FEB-2004 (first entry)
XX
XX Antibody heavy chain variable region VH_3-20.
XX
XX

```

```

KW Antibody; stability; solubility; antigen binding affinity;
XX variable region; human.
XX
XX Homo sapiens.
XX
XX WO2003074679-A2.
XX
XX 12-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-US006598.
XX
XX 01-MAR-2002; 2002US-0360843P.
XX
XX 29-MAY-2002; 2002US-0384197P.
XX
XX (XENC-) XENCOR.
XX
XX Lazar GA, Desjarlais JR, Marshall SA, Dahyat B;
XX
XX WPI; 2003-722066/68.
XX
XX Computer optimization of physicochemical properties of antibodies
XX comprises analyzing the interactions of amino acids at variable
XX positions.
XX
XX Example 16; Fig 40a; 135pp; English.
XX
XX The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
XX
SQ Sequence 98 AA;
XX
Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GINWNGSGTGYADSVKG 17
DB 50 GINWNGSGTGYADSVKG 66
XX
RESULT 10
ADP10024
ID ADF10024 standard; protein; 98 AA.
XX
XX ADF10024;
XX
XX 12-FEB-2004 (first entry)
XX
XX VEGF antibody heavy chain variable region VH_3-20.
XX
XX Antibody; stability; solubility; antigen binding affinity;
XX variable region; human; VEGF.
XX
XX Homo sapiens.
XX
XX WO2003074679-A2.
XX
XX 12-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-US006598.
XX

```

PR 01-MAR-2002; 2002US-0360843P.
 PR 29-MAY-2002; 2002US-0384197P.
 XX (XENC-) XENCOR.
 XX PA
 XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
 XX MPI; 2003-722066/58.
 DR
 PT Computer optimization of physicochemical properties of antibodies
 PT comprises analyzing the interactions of amino acids at variable
 PT positions.
 XX
 XX Example 6; Fig 16a; 135pp; English.
 CC The present invention relates to a method for optimizing at least one
 CC physico-chemical property of an antibody by a computational screening
 CC method. The method comprises: receiving a template antibody structure;
 CC selecting at least one variable position belonging to the antibody
 CC structure; selecting at least one amino acid to be considered at the
 CC variable position(s); analyzing the interaction of each selected amino
 CC acid at each variable position with at least part of the remainder of the
 CC antibody, including the selected amino acids at other variable positions;
 CC and identifying a set of at least one antibody sequence with at least one
 CC optimized physico-chemical property. The method is useful for optimizing
 CC the physico-chemical properties of an antibody, especially the stability,
 CC solubility, or antigen binding affinity. The optimized antibody may be
 CC useful for treating a patient. The present sequence is an antibody
 CC variable region sequence used to illustrate the invention.
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. No. 8.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17
 |||||
 Db 50 GINWNGSGTGYADSVKG 66

RESULT 11
 ADJ80300
 ID ADJ80300 standard; protein; 98 AA.
 XX
 AC ADJ80300;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 XX

XX VH gene locus antibody amino acid sequence #20.
 XX

XX hybrid antibody; antibody; framework region; homology; immunogenicity.
 KM

OS Homo sapiens.
 XX

PN WO2003048321-A2.
 XX

PD 12-JUN-2003.
 XX

PF 03-DEC-2002; 2002W0-US038450.
 XX

PR 03-DEC-2001; 2001US-0336591P.
 XX

PA (ALEX-) ALEXION PHARM INC.
 XX

PI Rother R, Wu D;
 XX

PI MPI; 2003-513753/48.
 XX

PT Producing a hybrid antibody or hybrid antibody fragment by operatively
 PT linking the selected framework sequences to one or more complementarily
 PT determining regions of the initial antibody.
 XX

PS Disclosure; SEQ ID NO 60; 77pp; English.

XX The invention relates to a method of producing a hybrid antibody or
 CC hybrid antibody fragment by: (i) providing an initial antibody having
 CC specificity for a target; (ii) determining the sequence of a variable
 CC region of the initial antibody; (iii) selecting a first component of the
 CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
 CC sequence of the first component to sequences contained in a reference
 CC database of antibody sequences or antibody fragment sequences from a
 CC target species; (v) selecting a sequence from an antibody in the database
 CC which demonstrates a high degree of homology to the first component; (vi)
 CC selecting a second component of the variable region which is different
 CC than the first component; the second component selected from the group
 CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
 CC second component to sequences contained in a reference database of
 CC antibody sequences or antibody fragment sequences from the target species
 CC; (viii) selecting a sequence from the database which demonstrates a high
 CC degree of homology to the second component and which is from a different
 CC antibody than the selected antibody; and (ix) operatively linking the
 CC selected framework sequences to one or more complementarily determining
 CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
 CC hybrid antibody fragment. The method is useful for producing a hybrid
 CC antibody or hybrid antibody fragment (claimed). The antibody and
 CC fragments are useful for therapeutic and diagnostic purposes. The method
 CC uses entire framework regions from a single antibody variable heavy or
 CC variable light chain to receive the CDRs. This produces antibodies that
 CC are highly homologous and exhibit reduced immunogenicity while
 CC maintaining an optimum binding profile. This sequence represents the
 CC amino acid sequence of an antibody from the VH gene locus.
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. No. 8.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17
 |||||
 Db 50 GINWNGSGTGYADSVKG 66

RESULT 12
 AAY95177
 ID AAY95177 standard; protein; 113 AA.
 XX
 AC AAY95177;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 XX

XX Anti-platelet glycoprotein Ib human H1b-1 VH.
 XX

XX Variable heavy chain; single chain antibody; scFv; human; H1b-1;
 KM glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KM antithrombotic; thrombus; therapy; diagnostic.
 XX

OS Homo sapiens.
 XX

XX
 XX

XX Key Location/Qualifiers
 FH Region 1.30
 FT Region /note= "framework region 1"
 FT Region 31..34
 FT Region /note= "complementarily determining region 1"
 FT Region 35..49
 FT Region /note= "framework region 2"
 FT Region 50..66
 FT Region /note= "complementarily determining region 2"
 FT Region 67..98
 FT Region /note= "framework region 3"
 FT Region 99..104
 FT Region /note= "complementarily determining region 3"
 FT Region 105..113
 FT Region /note= "framework region 4"
 XX

PN WO200026667-A1.
 XX
 PD 11-MAY-2000.
 XX
 XX 29-OCT-1999; 99WO-US025495.
 PF
 XX 30-OCT-1998; 98US-0106275P.
 XX
 PA (MILL/) MILLER J L.
 XX
 PI Miller JL;
 XX
 DR WPI; 2000-365744/31.
 DR N-PSDB; AAA27658.
 XX
 PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 PT Id alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.
 XX
 XX Claim 10; Page 71; 89pp; English.
 PS
 CC The present sequence is that of the heavy chain variable region (VH) of
 CC human single chain antibody (scFv) Hib-1 (see AAY95198), which is
 CC directed against platelet glycoprotein Ib (GPIb). The Hib series of scFv
 CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of
 CC phagemid selection against transfected CHO cells expressing the GPIb
 CC alpha component of the GPIb/IX/V complex on their surface, followed by a
 CC 4th round of selection against washed human platelets, and 2 final rounds
 CC in which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AAY95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by *Escherichia coli*, the Hib scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIb alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed
 CC
 CC Sequence 113 AA;
 SO
 Query Match 100.0%; Score 96; DB 3; Length 113;
 Best Local Similarity 100.0%; Pred. No. 9.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GINWNGSGTGYADSVKG 17
 |||||
 50 GINWNGSGTGYADSVKG 66
 DB
 RESULT 13
 AAY95178
 ID AAY95178 standard; protein; 113 AA.
 XX
 AC AAY95178;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Anti-platelet glycoprotein Ib human Hib-1 VH.
 XX
 KW Variable heavy chain; single chain antibody; scFv; human; Hib-1;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 1..30
 FT /note= "framework region 1"
 FT 31..34
 FT Region

FT /note= "complementarity determining region 1"
 FT 35..49
 FT /note= "framework region 2"
 FT 50..66
 FT /note= "complementarity determining region 2"
 FT 67..98
 FT /note= "framework region 3"
 FT 99..104
 FT /note= "complementarity determining region 3"
 FT 105..113
 FT /note= "framework region 4"
 FT
 PN WO200026667-A1.
 XX
 PD 11-MAY-2000.
 XX
 XX 29-OCT-1999; 99WO-US025495.
 PF
 XX 30-OCT-1998; 98US-0106275P.
 XX
 PA (MILL/) MILLER J L.
 XX
 PI Miller JL;
 XX
 DR WPI; 2000-365744/31.
 DR
 PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 PT Id alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.
 XX
 XX Claim 10; Page; 89pp; English.
 PS
 CC The present sequence is that of the heavy chain variable region (VH) of
 CC human single chain antibody (scFv) Hib-1 (see AAY95198), which is
 CC directed against platelet glycoprotein Ib (GPIb). The Hib series of scFv
 CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of
 CC phagemid selection against transfected CHO cells expressing the GPIb
 CC alpha component of the GPIb/IX/V complex on their surface, followed by a
 CC 4th round of selection against washed human platelets, and 2 final rounds
 CC in which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AAY95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by *Escherichia coli*, the Hib scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIb alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Note: The present sequence is
 CC not shown in the specification but is derived from the Hib-1 VH sequence
 CC given on page 71 (see AAY95177)
 CC
 CC Sequence 113 AA;
 SO
 Query Match 100.0%; Score 96; DB 3; Length 113;
 Best Local Similarity 100.0%; Pred. No. 9.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GINWNGSGTGYADSVKG 17
 |||||
 50 GINWNGSGTGYADSVKG 66
 DB
 RESULT 14
 AAY95189
 ID AAY95189 standard; protein; 115 AA.
 XX
 AC AAY95189;
 XX
 DT 29-AUG-2000 (first entry)

XX Anti-platelet glycoprotein Ib human H1b-1 VH. "

DE Variable heavy chain; single chain antibody; scFv; human; H1b-1;

XX glycoprotein Ib alpha, platelet; aggregation; antiaggregant;

KM antithrombotic; thrombus; therapy; diagnostic.

XX Homo sapiens.

OS

XX Key

XX Location/Qualifiers

FT Region 1..30

FT /note= "framework region 1"

FT 31..34

FT /note= "complementarity determining region 1"

FT 35..49

FT /note= "framework region 2"

FT 50..66

FT /note= "complementarity determining region 2"

FT 67..98

FT /note= "framework region 3"

FT 99..104

FT /note= "complementarity determining region 3"

FT 105..115

FT /note= "framework region 4"

XX WO20026667-A1.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025495.

XX 30-OCT-1998; 98US-0106275P.

XX (MILL/) MILLER J L.

XX Miller JL;

XX WPI; 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

PT Ib alpha molecule useful for producing antibodies which inhibit platelet

PT aggregation.

PS Claim 13; Fig 5; 89pp; English.

XX

XX The present sequence is that of the heavy chain variable region (VH) of

CC human single chain antibody (scFv) H1b-1 (see AAY95198), which is

CC directed against platelet glycoprotein Ib (GPIb). The H1b series of scFv

CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of

CC phageid selection against transfected CHO cells expressing the GPIb

CC alpha component of the GPIb/IX/V complex on their surface, followed by a

CC 4th round of selection against washed human platelets, and 2 final rounds

CC in which attempts were made to displace scFv from washed platelets by

CC flooding with murine monoclonal antibody or mimotope peptide (see

CC AAY95229). Whether displayed as surface proteins on a phageid or

CC secreted as free scFv by Escherichia coli, the H1b scFv clones are

CC capable of inhibiting von Willebrand factor-dependent aggregation of

CC platelets. The scFv are composed of native human protein sequences and

CC are therefore attractive potential reagents for therapeutic purposes.

CC They provide a new class of antithrombotic agents, useful for the

CC prevention of platelet-dependent thrombi in diseased arteries, bypass

CC grafts, dialysis etc., and can also be used as diagnostic reagents.

CC Methods of inhibiting aggregation of platelets, of binding human platelet

CC GPIb alpha and of selecting a VH or VL region of an antibody that

CC inhibits platelet aggregation are claimed

XX

SQ Sequence 115 AA;

Query Match 100.0%; Score 96; DB 3; Length 115;

Best Local Similarity 100.0%; Pred. No. 97e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINMGSTGYADSVKG 17

DB 50 GINMGSTGYADSVKG 66

RESULT 15

AAAY95190

ID AAY95190 standard; protein, 115 AA.

XX

XX AAY95190;

XX 29-AUG-2000 (first entry)

XX

XX Anti-platelet glycoprotein Ib human H1b-1 VH.

DE

XX

XX Variable heavy chain; single chain antibody; scFv; human; H1b-1;

KM glycoprotein Ib alpha; platelet; aggregation; antiaggregant;

KM antithrombotic; thrombus; therapy; diagnostic.

XX

OS Homo sapiens.

XX

XX Key

XX Location/Qualifiers

FT Region 1..30

FT /note= "framework region 1"

FT 31..34

FT /note= "complementarity determining region 1"

FT 35..49

FT /note= "framework region 2"

FT 50..66

FT /note= "complementarity determining region 2"

FT 67..98

FT /note= "framework region 3"

FT 99..104

FT /note= "complementarity determining region 3"

FT 105..115

FT /note= "framework region 4"

XX WO20026667-A1.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025495.

XX 30-OCT-1998; 98US-0106275P.

XX (MILL/) MILLER J L.

XX Miller JL;

XX WPI; 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

PT Ib alpha molecule useful for producing antibodies which inhibit platelet

PT aggregation.

PS Claim 13; Page; 89pp; English.

XX

XX The present sequence is that of the heavy chain variable region (VH) of

CC human single chain antibody (scFv) H1b-1 (see AAY95198), which is

CC directed against platelet glycoprotein Ib (GPIb). The H1b series of scFv

CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of

CC phageid selection against transfected CHO cells expressing the GPIb

CC alpha component of the GPIb/IX/V complex on their surface, followed by a

CC 4th round of selection against washed human platelets, and 2 final rounds

CC in which attempts were made to displace scFv from washed platelets by

CC flooding with murine monoclonal antibody or mimotope peptide (see

CC AAY95229). Whether displayed as surface proteins on a phageid or

CC secreted as free scFv by Escherichia coli, the H1b scFv clones are

CC capable of inhibiting von Willebrand factor-dependent aggregation of

CC platelets. The scFv are composed of native human protein sequences and

CC are therefore attractive potential reagents for therapeutic purposes.

CC They provide a new class of antithrombotic agents, useful for the

CC prevention of platelet-dependent thrombi in diseased arteries, bypass

CC grafts, dialysis etc., and can also be used as diagnostic reagents.

CC

CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIIb alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Note: The present sequence is
 CC not shown in the specification but is derived from the H1b-1 VH sequence
 CC given in Fig 5 (see AA195189)
 XX
 SQ Sequence 115 AA;

Query Match 100.0%; Score 96; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGSTGYADSVKXG 17
 |||||
 Db 50 GINWNGSGSTGYADSVKXG 66

Search completed: April 25, 2005, 20:22:29
 Job time : 11.4224 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 2.61973 Seconds

(without alignments)
484,413 Million cell updates/sec

Title: US-10-029-926d-115

Perfect score: 96

Sequence: 1 GINMNGSTGYADSVKVG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfileal.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	116	2	US-08-652-816A-14
2	96	100.0	117	3	US-08-545-809A-106
3	96	100.0	309	3	US-09-079-029-9
4	79	82.3	117	4	US-09-424-840B-109
5	79	82.3	118	3	US-08-545-809A-97
6	79	82.3	119	4	US-09-840-459-88
7	79	82.3	119	4	US-09-497-625A-88
8	79	82.3	120	2	US-08-958-201-8
9	79	82.3	120	2	US-08-958-201-10
10	74	77.1	149	4	US-08-471-276-898
11	71	74.0	17	4	US-08-424-840B-114
12	71	74.0	117	3	US-08-545-809A-119
13	71	74.0	118	3	US-08-545-809A-125
14	71	74.0	124	4	US-09-424-840B-123
15	68	70.8	117	1	US-07-942-245-24
16	68	70.8	126	4	US-09-232-290-35
17	66	68.8	17	4	US-09-424-840B-70
18	66	68.8	17	4	US-09-424-840B-78
19	66	68.8	124	4	US-09-424-840B-123
20	63	65.6	126	3	US-08-983-607-26
21	62.5	65.1	117	3	US-09-157-370-1
22	62	64.6	17	1	US-08-264-093-22
23	62	64.6	89	4	US-09-840-459-48
24	62	64.6	89	4	US-09-497-625A-48
25	62	64.6	111	4	US-09-899-896-7
26	62	64.6	118	2	US-08-652-816A-11
27	62	64.6	120	1	US-08-264-093-14

28	62	64.6	268	4	US-09-976-118-1	Sequence 1, Appl
29	62	64.6	483	3	US-09-049-672A-5	Sequence 5, Appl
30	61.5	64.1	95	3	US-09-043-514-2	Sequence 2, Appl
31	61.5	64.1	116	3	US-08-545-809A-135	Sequence 135, App
32	61	63.5	113	3	US-08-974-899-6	Sequence 6, Appl
33	61	63.5	113	4	US-09-795-798-6	Sequence 6, Appl
34	61	63.5	116	3	US-09-184-658-48	Sequence 48, Appl
35	61	63.5	116	3	US-08-983-607-36	Sequence 36, Appl
36	61	63.5	116	4	US-09-504-262D-48	Sequence 48, Appl
37	61	63.5	116	4	US-09-840-459-80	Sequence 80, Appl
38	61	63.5	116	4	US-09-497-625A-80	Sequence 80, Appl
39	61	63.5	117	3	US-08-545-809A-103	Sequence 103, App
40	61	63.5	117	3	US-08-545-809A-109	Sequence 109, App
41	61	63.5	117	3	US-08-983-607-46	Sequence 46, Appl
42	61	63.5	117	4	US-09-840-459-83	Sequence 83, Appl
43	61	63.5	117	4	US-09-497-625A-83	Sequence 83, Appl
44	61	63.5	118	2	US-08-652-816A-12	Sequence 12, Appl
45	61	63.5	119	4	US-09-648-067A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-652-816A-14
; Sequence 14, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:

```

RESULT 4
US-09-424-840B-109
; Sequence 109, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-SPB18/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19733904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 17
; TYPE: PRT

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```

; ORGANISM: Homo sapiens
US-09-424-840B-109

Query Match      82.3%; Score 79; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GINWNGSGTGYADSVKG 17
Db      1 GISMNGSGTGYADSVKG 17

RESULT 5
US-08-545-809A-97
; Sequence 97, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tsauku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-97

Query Match      82.3%; Score 79; DB 3; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.00061;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GINWNGSGTGYADSVKG 17
Db      69 GISMNGSGTGYADSVKG 85

RESULT 6
US-09-840-459-88
; Sequence 88, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter

```

```

; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-88

Query Match      82.3%; Score 79; DB 4; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00061;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GINWNGSGTGYADSVKG 17
Db      50 GISMNGSGTGYADSVKG 66

RESULT 7
US-09-497-625A-88
; Sequence 88, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-88

Query Match      82.3%; Score 79; DB 4; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00061;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GINWNGSGTGYADSVKG 17
Db      50 GISMNGSGTGYADSVKG 66

RESULT 8
US-08-958-201-8
; Sequence 8, Application US/08958201

```

```
/ Patent No. 5977319
/ GENERAL INFORMATION:
/ APPLICANT: Pope, Anthony R
/ APPLICANT: Pritchard, Kevin
/ APPLICANT: Williams, Andrew J
/ APPLICANT: Johnson, Kevin S
/ TITLE OF INVENTION: Specific binding members for estradiol;
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/958,201
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/028,897
/ FILING DATE: 21-OCT-1996
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: 2D
/
/ US-08-958-201-8
/
Query Match      82.3%; Score 79; DB 2; Length 120;
Best Local Similarity 82.4%; Pred. No. 0.00062;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GINWNGSTGYADSVKG 17
Db      50 GISMNSGSIQYADSVKG 66

RESULT 9
US-08-958-201-10
/ Sequence 10, Application US/08958201
/ Patent No. 5977319
/ GENERAL INFORMATION:
/ APPLICANT: Pope, Anthony R
/ APPLICANT: Pritchard, Kevin
/ APPLICANT: Williams, Andrew J
/ APPLICANT: Johnson, Kevin S
/ TITLE OF INVENTION: Specific binding members for estradiol;
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/958,201
/ FILING DATE:
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 60/028,897
/ FILING DATE: 21-OCT-1996
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: 2Db
/
/ US-08-958-201-10
/
Query Match      82.3%; Score 79; DB 2; Length 120;
Best Local Similarity 82.4%; Pred. No. 0.00062;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GINWNGSTGYADSVKG 17
Db      50 GISMNSGSIQYADSVKG 66

RESULT 10
US-09-471-276-898
/ Sequence 898, Application US/09471276
/ Patent No. 6822072
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.025CPI
/ CURRENT APPLICATION NUMBER: US/09/471,276
/ CURRENT FILING DATE: 1999-12-21
/ EARLIER APPLICATION NUMBER: 09/057,719
/ EARLIER FILING DATE: 1998-04-09
/ EARLIER APPLICATION NUMBER: 09/069,047
/ EARLIER FILING DATE: 1998-04-28
/ EARLIER APPLICATION NUMBER: PCT/IB99/00712
/ EARLIER FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 1622
/ SOFTWARE: Patent.pm
/ SEQ ID NO 898
/ LENGTH: 149
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: -19..-1
/
/ US-09-471-276-898
/
Query Match      77.1%; Score 74; DB 4; Length 149;
Best Local Similarity 76.5%; Pred. No. 0.0039;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GINWNGSTGYADSVKG 17
Db      69 GITWNSGXIQYADSVKG 85

RESULT 11
US-09-424-840B-114
/ Sequence 114, Application US/09424840B
/ Patent No. 679038
/ GENERAL INFORMATION:
/ APPLICANT: Berchold, Peter
/ APPLICANT: Escher, Robert F. A.
/ TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
/ FILE REFERENCE: 100564-09049
/ CURRENT APPLICATION NUMBER: US/09/424,840B
/ CURRENT FILING DATE: 1999-12-03
/ PRIOR APPLICATION NUMBER: DE 19820663.1
/ PRIOR FILING DATE: 1998-05-08
/ PRIOR APPLICATION NUMBER: DE 19755227.7
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;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: DE 19723904.8
;; PRIOR FILING DATE: 1997-06-06
;; NUMBER OF SEQ ID NOS: 128
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 114
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-424-840B-114

Query Match 74.0%; Score 71; DB 4; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.0011;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17
DB 1 GISWDSGTIGYADSVKG 17

RESULT 12

US-08-545-809A-119
; Sequence 119, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tadaaki
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-119

Query Match 74.0%; Score 71; DB 3; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.008;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17
DB 69 GWSWNGSTGYADSVKG 85

RESULT 13

US-08-545-809A-125
; Sequence 125, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tadaaki
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-125

Query Match 74.0%; Score 71; DB 3; Length 118;
Best Local Similarity 81.2%; Pred. No. 0.0081;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 INWNGSTGYADSVKG 17
DB 70 ISWDSGTGYADSVKG 85

RESULT 14

US-09-424-840B-18
; Sequence 18, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchold, Peter
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18

LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-18

Query Match 74.0%; Score 71; DB 4; Length 124;
Best Local Similarity 70.6%; Pred. No. 0.0085;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 GINWNGSTGYADSVKG 17
Db 50 GISWDSSTGYADSVKG 66

RESULT 15
US-07-942-245-24
Sequence 24, Application US/07942245
Patent No. 563641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-24

Query Match 70.8%; Score 68; DB 1; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.021;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 GINWNGSTGYADSVKG 17
Db 50 GISWDSSTGYADSVKG 66

Search completed: April 25, 2005, 21:12:14
Job time : 3.61973 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 7.51996 Seconds

(without alignments)
752.325 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSTGYADSVKVG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

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20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	17	US-10-032-037B-115	Sequence 115, App
2	96	100.0	17	US-10-029-988B-115	Sequence 115, App
3	96	100.0	17	US-10-032-423A-115	Sequence 115, App
4	96	100.0	17	US-10-029-926B-115	Sequence 115, App
5	96	100.0	17	US-10-194-975-20	Sequence 20, Appl
6	96	100.0	17	US-10-194-975-20	Sequence 20, Appl
7	96	100.0	17	US-10-108-817-60	Sequence 60, Appl
8	96	100.0	17	US-10-032-037B-61	Sequence 61, Appl
9	96	100.0	17	US-10-029-988B-61	Sequence 61, Appl
10	96	100.0	17	US-10-032-423A-61	Sequence 61, Appl
11	96	100.0	17	US-10-453-698-60	Sequence 60, Appl
12	96	100.0	17	US-10-029-926B-61	Sequence 61, Appl
13	96	100.0	17	US-10-379-392-21	Sequence 21, Appl
				US-10-884-830-599	Sequence 599, App

14	96	100.0	122	US-10-447-331-6	Sequence 6, Appl1
15	96	100.0	239	US-09-880-748-937	Sequence 937, App
16	96	100.0	239	US-09-880-748-2015	Sequence 2015, App
17	96	100.0	239	US-09-880-748-2038	Sequence 2038, App
18	96	100.0	239	US-10-293-418-937	Sequence 937, App
19	96	100.0	239	US-10-293-418-2015	Sequence 2015, App
20	96	100.0	239	US-10-293-418-2038	Sequence 2038, App
21	96	100.0	242	US-10-935-290-130	Sequence 130, App
22	96	100.0	244	US-10-322-673-42	Sequence 42, Appl
23	96	100.0	249	US-10-935-290-40	Sequence 40, Appl
24	96	100.0	266	US-10-032-037B-204	Sequence 204, App
25	96	100.0	266	US-10-029-988B-204	Sequence 204, App
26	96	100.0	266	US-10-032-423A-204	Sequence 204, App
27	96	100.0	277	US-10-032-037B-25	Sequence 25, App
28	96	100.0	277	US-10-032-037B-203	Sequence 203, App
29	96	100.0	277	US-10-029-988B-25	Sequence 25, App
30	96	100.0	277	US-10-029-988B-203	Sequence 203, App
31	96	100.0	277	US-10-032-423A-25	Sequence 25, App
32	96	100.0	277	US-10-032-423A-203	Sequence 203, App
33	96	100.0	277	US-10-029-926B-25	Sequence 25, App
34	96	100.0	277	US-10-029-926B-203	Sequence 203, App
35	96	100.0	280	US-10-880-922-5	Sequence 5, Appl1
36	96	100.0	280	US-10-880-922-6	Sequence 6, Appl1
37	96	100.0	280	US-10-880-922-55	Sequence 55, Appl1
38	96	100.0	280	US-10-880-922-56	Sequence 56, Appl1
39	96	100.0	280	US-10-880-922-60	Sequence 60, Appl1
40	96	100.0	280	US-10-880-922-61	Sequence 61, Appl1
41	96	100.0	309	US-10-052-798-9	Sequence 9, Appl1
42	96	100.0	309	US-10-288-917-9	Sequence 9, Appl1
43	96	100.0	309	US-10-423-448-9	Sequence 9, Appl1
44	96	100.0	464	US-10-032-037B-26	Sequence 26, Appl1
45	96	100.0	464	US-10-029-988B-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1

US-10-032-037B-115

Sequence 115, Application US/10032037B

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOETIFES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

PRIOR FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 115

LENGTH: 17

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-037B-115

Query Match 100.0%; Score 96; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GINWNGSTGYADSVKVG 17

1 GINWNGSTGYADSVKVG 17

RESULT 2

US-10-029-988B-115

Sequence 115, Application US/10029988B

Publication No. US20040001839A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

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; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-115

Query Match          100.0%; Score 96; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
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Db      1 GINWNGSGTGYADSVKG 17

RESULT 3
US-10-032-423A-115
; Sequence 115, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-115

Query Match          100.0%; Score 96; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
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Db      1 GINWNGSGTGYADSVKG 17

RESULT 4
US-10-029-926B-115
; Sequence 115, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-115
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Query Match          100.0%; Score 96; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
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Db      1 GINWNGSGTGYADSVKG 17

RESULT 5
US-10-194-975-20
; Sequence 20, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-20

Query Match          100.0%; Score 96; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
        |||||
Db      50 GINWNGSGTGYADSVKG 66

RESULT 6
US-10-308-817-60
; Sequence 60, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rothen, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-60

Query Match          100.0%; Score 96; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
        |||||
Db      50 GINWNGSGTGYADSVKG 66

RESULT 7
US-10-032-037B-61
; Sequence 61, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
US-10-032-037B-61
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Query Match      100.0%; Score 96; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
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```
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Nahiyat, Basail I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-379-392-21
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Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GINMNGSTGYADSVKG 17
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Db      50 GINMNGSTGYADSVKG 66
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RESULT 13
US-10-884-830-599
Sequence 599, Application US/10884830
Publication No. US2005004354A1
GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT APPLICATION NUMBER: US/10/884,830
CURRENT FILING DATE: 2004-07-01
PRIOR APPLICATION NUMBER: US/09/534,717
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/126,603
PRIOR FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 599
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-884-830-599
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Query Match          100.0%; Score 96; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GINMNGSTGYADSVKG 17
      |||||
Db      50 GINMNGSTGYADSVKG 66
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RESULT 14
US-10-447-331-6
Sequence 6, Application US/10447331
Publication No. US20030219434A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
FILE REFERENCE: GENENT.122A
CURRENT APPLICATION NUMBER: US/10/447,331
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: US/09/515,825
PRIOR FILING DATE: 2000-02-29
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PRIOR APPLICATION NUMBER: 60/122262
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 122
TYPE: PRT
ORGANISM: Homo sapiens
US-10-447-331-6
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Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GINMNGSTGYADSVKG 17
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Db      50 GINMNGSTGYADSVKG 66
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RESULT 15
US-09-880-748-937
Sequence 937, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 937
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-937
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Query Match          100.0%; Score 96; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
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QY      1 GINMNGSTGYADSVKG 17
      |||||
Db      50 GINMNGSTGYADSVKG 66
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Search completed: April 25, 2005, 21:09:48
Job time : 7.51996 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 1.96009 Seconds
(without alignments)
834.495 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96
Sequence: 1 GINMNGSTGYADSVK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	98	2	S26928 Ig heavy chain V r
2	87	90.6	112	2	PH1654 Ig heavy chain V r
3	79	82.3	98	2	S26927 Ig heavy chain V r
4	79	82.3	121	2	S31104 Ig heavy chain (su
5	79	82.3	128	2	S31595 Ig heavy chain V r
6	76	79.2	123	2	S30532 Ig heavy chain V r
7	74	77.1	121	2	S31118 Ig heavy chain - h
8	73	76.0	100	2	S69896 Ig heavy chain V r
9	71	74.0	98	2	S26934 Ig heavy chain V r
10	71	74.0	98	2	S26929 Ig heavy chain V r
11	71	74.0	120	2	S44111 Ig heavy chain V-D
12	71	74.0	191	2	JL0048 Ig heavy chain V r
13	69	71.9	120	1	GIHDB Ig heavy chain V-I
14	68	70.8	145	2	S11239 Ig heavy chain V r
15	65	67.7	120	2	S31273 Ig heavy chain V r
16	65	67.7	123	2	PC4281 anti-SS-A/Ro 60K p
17	64	66.7	90	2	S24248 Ig heavy chain V r
18	64	66.7	120	2	S26278 Ig heavy chain V r
19	62	64.6	96	2	S20781 Ig heavy chain V r
20	61.5	64.1	97	2	S26935 Ig heavy chain V r
21	61.5	64.1	97	2	S46462 Ig heavy chain V r
22	61.5	64.1	116	2	B28966 Ig heavy chain pre
23	61.5	64.1	116	2	S31110 Ig heavy chain - h
24	61.5	64.1	146	2	I47184 Ig heavy chain var
25	61	63.5	98	2	S26889 Ig heavy chain V r
26	61	63.5	98	2	S54856 Ig heavy chain V r
27	61	63.5	99	2	S24259 Ig heavy chain V r
28	61	63.5	100	2	S24258 Ig heavy chain V r
29	61	63.5	101	2	S24257 Ig heavy chain V r

30	61	63.5	102	2	S24260 Ig heavy chain V r
31	61	63.5	104	2	S24255 Ig heavy chain V r
32	61	63.5	105	2	S24249 Ig heavy chain V r
33	61	63.5	106	2	S24256 Ig heavy chain V r
34	61	63.5	108	2	PH1648 Ig heavy chain V r
35	61	63.5	109	2	S24254 Ig heavy chain V r
36	61	63.5	109	2	PH1649 Ig heavy chain V r
37	61	63.5	109	2	PH1649 Ig heavy chain V r
38	61	63.5	110	2	S24250 Ig heavy chain V r
39	61	63.5	112	2	PH1647 Ig heavy chain V r
40	61	63.5	113	2	S24247 Ig heavy chain V r
41	61	63.5	115	2	S09382 Ig heavy chain - c
42	61	63.5	117	2	A45953 Ig heavy chain pre
43	61	63.5	118	2	S31121 Ig heavy chain - h
44	61	63.5	119	2	D36005 Ig heavy chain V r
45	61	63.5	119	2	S31107 Ig heavy chain - h

ALIGNMENTS

RESULT 1
S26928 Ig heavy chain V region (DP-32) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26928
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A/Reference number: S26985; MUID:93021117; PMID:1404388
A/Accession: S26928
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <TD>
A/Cross-references: EMBL:Z12334; NID:G32887; PIDN:CAA78204.1; PID:G32888
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 96; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINMNGSTGYADSVK 17
DB 50 GINMNGSTGYADSVK 66

RESULT 2

PH1654 Ig heavy chain V region (clone 6H9) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1654
R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Saaso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphy-
A/Reference number: PH1642; MUID:9301610; PMID:8315388
A/Accession: PH1654
A/Molecule type: mRNA
A/Residues: 1-112 <HIL>
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 87; DB 2; Length 112;
Best Local Similarity 94.1%; Pred. No. 4.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GINMNGSTGYADSVK 17
DB 50 GINMNGSTGYADSVK 66

Db 42 GINWNGSTGYADSVKG 58

RESULT 3

Ig heavy chain V region (DP-31) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S26927

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:1404388

A/Accession: S26927

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: EMBL:Z12333; NID:932885; PIRN:CAA78203.1; PID:932886

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 79; DB 2; Length 98;

Best Local Similarity 82.4%; Pred. No. 6.2e-05;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17

Db 50 GINWNGSTGYADSVKG 66

RESULT 4

Ig heavy chain (subclass IgM) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999

C/Accession: S31104

R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A/Reference number: S31104; MUID:9211633; PMID:1730252

A/Accession: S31104

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-121 <RAA>

A/Cross-references: EMBL:X63080; NID:932846; PIRN:CAA44802.1; PID:932647

C/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 79; DB 2; Length 121;

Best Local Similarity 82.4%; Pred. No. 7.7e-05;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17

Db 50 GINWNGSTGYADSVKG 66

RESULT 5

S31595

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31595

R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31595

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <CUI>

A/Cross-references: EMBL:Z14171; NID:931007; PIRN:CAA78540.1; PID:931008

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/23-106/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 79; DB 2; Length 128;

Best Local Similarity 82.4%; Pred. No. 8.1e-05;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17

Db 58 GINWNGSTGYADSVKG 74

RESULT 6

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S30532

R/Mariette, X.

submitted to the EMBL Data Library, October 1992

A/Reference number: S30532

A/Accession: S30532

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-123 <MAR>

A/Cross-references: UNIPROT:Q8MU18; EMBL:Z18318

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 76; DB 2; Length 123;

Best Local Similarity 76.5%; Pred. No. 0.00022;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17

Db 50 GINWNGSTGYADSVKG 66

RESULT 7

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31118

R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A/Reference number: S31104; MUID:9211633; PMID:1730252

A/Accession: S31118

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-121 <RAA>

A/Cross-references: EMBL:X62969

C/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 74; DB 2; Length 121;

Best Local Similarity 76.5%; Pred. No. 0.00044;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17

Db 50 GINWNGSTGYADSVKG 66

RESULT 8

S69896

Ig heavy chain/region (clone RFKLSH), rheumatoid factor - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: S69896
R:Randem, I., Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capria, D.U.; Natvig, J.
Eur. J. Immunol. 23, 1220-1225, 1993
A>Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune response
A:Reference number: S69896, MUID:93272805, PMID:8500520
A:Accession: S69896
A:Status: preliminary/ translation not shown
A:Molecule type: mRNA
A:Residues: 1-100 <RAN>
A:Cross-references: EMBL:X73605; NID:G509797; PIRN:CA51998.1; PID:G509798
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology <IMM>
F:1-98/Domain: immunoglobulin homology

Query Match	76.0%	Score 73;	DB 2;	Length 100;
Best Local Similarity	76.5%	Pred. No. 0.00051;		
Matches 13; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      1 GINWNGSTGYADSVKG 17
          ||| | | | | | |
Db      50 GITWNSGRIGYADSVKG 66
```

RESULT 9

Ig heavy chain V region (DP-59) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26934
R:Tolsonson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12359; NID:G32937; PIDN:CAA78229.1; PID:G32938
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match	74.0%	Score 71	DB 2	Length 98
Best Local Similarity	70.6%	Pred. No. 0.001		
Matches	12	Conservative	2	Mismatches 3
				Indels 0
				Gaps 0
QY	1	GINMGSGTGADSVYG	17	
		:::		
db	50	GVSWMGSRTHYADSVYG	66	

RESULT 10
S26929

Ig heavy chain/region (DP-33) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26929
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26929
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: EMBL:Z12335; NID:G32889; PIDD:CA78205.1; PID:G32890
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 71; DB 2; Length 98;

Best Local Similarity 81.2%; Pred. No. 0.001;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY      2 INWNGSGTGYADSVKG 17
      ||:||||| |||||
Db      51 ISWDGGSTYYADSVKG 66
```

RESULT 11

Ig heavy chain V-D-J region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
A/Accession: S44111
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A/Reference number: S44105
A/Accession: S44111
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <HAW>
A/Cross-references: EMBL: Z31387, NID: G472965, PIDN: CAA83262.1; PID: G940522
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
;15-98/Domain: immunoglobulin homology <IMM>

Query Match	74.0%;	Score 71;	DB 2;	Length 120
Best Local Similarity	81.2%;	Pred. No. 0.0012;		
Matches 13;	Conservative 2;	Mismatches 1;	Indels	

```
QY      2 INWNGSGTGYADSVKG 17
          |::||| | |||||
Db      51 ISWDGGSTYYADSVKG 66
```

RESULT 12

IG heavy chain V region precursor (clone cR19) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 15-Mar-2004
C:Accession: J100048; S66433
R:Baer, R.; Forster, A.; Lavenir, I.; Rabbits, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new
A:Reference number: J100047; MUID:88258392; PMID:3133445
A:Accession: J100048
A:Molecule type: mRNA
A:Residues: 1-191 <BEA>
A:Note: the authors translated the reading frame which extends to the stop codon; the s
A:Note: this sequence belongs to the VH III subgroup
R:Mueller-Newen, G.; Koehn, C.; Keul, R.; Hermann, U.; Mueller-Eberhard, W.; Wijdens, J
Eur. J. Biochem. 236, 837-842, 1996
A:Title: Purification and characterization of the soluble interleukin-6 receptor from h
A:Reference number: S66433; MUID:96270733; PMID:8665902
A:Accession: S66433
A:Molecule type: protein
A:Residues: 9-18 <MUB>
C:Keywords: heterotetramer; immunoglobulin
C:23-106/Domain: immunoglobulin homology <IMM>

Query Match	74.0%	Score 71	DB 2	Length 191
Best Local Similarity	70.6%	Pred. NC	0.002	
Matches 12, Conservative	2	Mismatches	3	Indels 0; Gaps 0

Qy	1	GINWNGSTGYADSVKG	17
	::		
Db	58	GVSWNGSRTHYADSVKG	74

RESULT 13

Ig heavy chain V-III region (Dob) - human

C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1979 #sequence_revision 31-Dec-1979 #text_change 09-Jul-2004
 C/Accession: A90431; A02065
 R/Steiner, L.A.; Garcia Pardo, A.; Margolies, M.N.
 Biochemistry 18, 4068-4080, 1979
 A/Title: Amino acid sequence of the heavy-chain variable region of the crystallizable hu
 A/Reference number: A90431; MUID:80020921; PMID:114209
 A/Accession: A90431
 A/Molecule type: protein
 A/Residues: 1-120 <STR>
 A/Cross-references: UNIPROT:P01782
 R/Steiner, L.A.; Lopes, A.D.
 Biochemistry 18, 4054-4067, 1979
 A/Title: The crystallizable human myeloma protein Dob has a hinge-region deletion.
 A/Reference number: A90430; MUID:80020920; PMID:114208
 A/Contents: annotation
 A/Note: this gamma-1 myeloma protein has a deletion in the hinge region; there are no 1
 C/Genetics:
 A/Gene: GDB:IGHV@
 A/Cross-references: GDB:128528; OMIM:147070
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:22-96/Disulfide bonds: #status predicted

Query Match 71.9%; Score 69; DB 1; Length 120;
 Best Local Similarity 81.2%; Pred. No. 0.0025;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GINMNGSGTGYADSVKG 17
 |||:| |||||
 DB 51 ITWNGSGVLADSVKG 66

RESULT 14

S11239
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S11239
 R/Felgenhauer, M.; Kohl, J.; Rueker, F.
 Nucleic Acids Res. 18, 4927, 1990
 A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
 A/Reference number: S11239; MUID:90370490; PMID:1697678
 A/Accession: S11239
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-145 <PEL>
 A/Cross-references: EMBL:X53613; NID:923865; PIDN:CAA37675.1; PID:9762936
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 68; DB 2; Length 145;
 Best Local Similarity 70.6%; Pred. No. 0.0042;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINMNGSGTGYADSVKG 17
 |||:| |||||
 DB 69 GISWSSSIGYADSVKG 85

RESULT 15

S36273
 Ig heavy chain V region (clone alpha-THY-32) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C/Accession: S36273
 R/Giffiths, A.D.; Malmqvist, M.; Marts, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.
 A/Reference number: S36256; MUID:91178448; PMID:7679990

A/Accession: S36273
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-120 <GRI>
 A/Cross-references: EMBL:Z18834; NID:933116; PIDN:CAA79286.1; PID:9939896
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 65; DB 2; Length 120;
 Best Local Similarity 76.5%; Pred. No. 0.0099;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINMNGSGTGYADSVKG 17
 |||:| |||||
 DB 50 GISWSSSIGYADSVKG 66

Search completed: April 25, 2005, 20:24:11
 Job time : 2.96009 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: April 25, 2005, 20:10:00 ; Search time 8.78271 Seconds
(without alignments)
991.192 Million cell updates/sec

Title: US-10-029-926D-115
Perfect score: 96
Sequence: 1 GINWNGSTGYADSVKXG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	112	2	Q9HCC1
2	84	87.5	499	2	Q8NSK4
3	82	85.4	494	2	Q6ZM64
4	79	82.3	104	2	Q9UL87
5	79	82.3	573	2	Q8WU38
6	73	76.0	472	2	Q6N089
7	69	71.9	120	1	HV3U HUMAN
8	61.5	64.1	116	1	HV05_CARAU
9	61	63.5	121	2	Q9UL71
10	61	63.5	593	2	Q6INM5
11	61	63.5	597	2	Q96B89
12	61	63.5	614	2	Q6DDQ7
13	60	62.5	584	2	Q6INK3
14	59	61.5	117	1	HV53 MOUSE
15	59	61.5	493	2	Q6GKX2
16	57	59.4	117	1	HV3C_HUMAN
17	56	58.3	118	2	Q9UL72
18	55	56.8	479	2	Q91WP5
19	54.5	56.8	466	2	Q6INW8
20	54	55.2	112	2	Q9UJCP3
21	53	55.2	115	1	HV3F_HUMAN
22	52	54.2	493	2	Q68CN4
23	51	53.1	121	1	HV3J_HUMAN
24	51	53.1	469	2	Q9FDT2
25	51	53.1	475	2	Q6MZQ6
26	51	53.1	838	2	Q7UVV9
27	50.5	52.6	97	1	HV56_MOUSE
28	50	52.1	874	2	Q6CK84
29	49	51.0	767	2	Q9U234
30	49	51.0	1089	2	Q64U63
31	48.5	50.5	117	1	HV02_CANFA

32	48	50.0	99	2	Q6B743	Q6B743	oryctolagus
33	48	50.0	117	1	HV55_MOUSE	P18526	mus musculus
34	48	50.0	119	1	HV31_HUMAN	P01773	homo sapien
35	48	50.0	279	2	Q9WZJ8	Q9WZJ8	thermocoga
36	48	50.0	298	2	Q9XGB4	Q9XGB4	trifolium r
37	48	50.0	416	2	Q9NPP6	Q9NPP6	homo sapien
38	48	50.0	469	2	Q8PD28	Q8PD28	xanthomonas
39	48	50.0	473	2	Q91205	Q91205	mus musculus
40	48	50.0	475	2	Q6GWM7	Q6GWM7	homo sapien
41	48	50.0	654	2	Q86AX3	Q86AX3	dictyosteli
42	48	50.0	761	2	Q20898	Q20898	caenorhabdi
43	48	50.0	4342	2	Q91157	Q91157	pseudomonas
44	47.5	49.5	100	2	Q6B755	Q6B755	oryctolagus
45	47	49.0	87	2	Q7Y3K4	Q7Y3K4	enterobacte

ALIGNMENTS

RESULT 1									
ID	Q9HCC1	PRELIMINARY;	PRT;	112 AA.					
AC	Q9HCC1;								
DT	01-MAR-2001 (TREMBLrel. 16, Created)								
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
DE	Single chain Fv (Fragment).								
OS	Homo sapiens (human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_Taxid=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;								
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AB049915; BAB16829.1; -								
DR	HSSP; P01783; IIGC.								
DR	InterPro; IPR007110; IG-Like.								
DR	InterPro; IPR003596; IG_V.								
DR	SMART; SM00406; IGV; 1.								
DR	PROSITE; PSS0835; IG_LIKE; 1.								
FT	NON TER	1	1						
FT	NON TER	112	112						
SQ	SEQUENCE	112 AA;	12243 MW;	24F1A45EC3B84788	CRC64;				
Query Match									
Best Local Similarity		100.0%;		Score 96;		DB 2;		Length 112;	
Matches 17; Conservative		100.0%;		Pred. No. 4.8e-07;					
		0; Mismatches		0; Indels		0; Gaps		0;	
OY	1 GINWNGSGTGYADSVKG 17								
Db	50 GINWNGSGTGYADSVKG 66								
RESULT 2									
ID	Q8NSK4	PRELIMINARY;	PRT;	499 AA.					
AC	Q8NSK4;								
DT	01-OCT-2002 (TREMBLrel. 22, Created)								
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)								
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)								
DE	MGC2165 protein.								
OS	Homo sapiens (human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_Taxid=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Blood;								
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klauser R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.;								

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusita K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pirange C.,
 RA Raha S.S., Loggellano N.A., Peters G.U., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.R., Gunaratne P.H.,
 RA Richardson S., Wolley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyaniak M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.,
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032249; AA32249.1; -.
 DR HSSP; P01876; IOM0.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 87.5%; Score 84; DB 2; Length 499;
 Best Local Similarity 93.8%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 INNMGSTGYADSVKG 17
 Db 70 INNMGSTGYADSVKG 85

RESULT 3
 Q6ZW64 PRELIMINARY; PRT; 494 AA.
 ID Q6ZW64
 AC Q6ZW64
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ41552.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Oca T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamaoka H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagaatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
 RA Masuno Y., Nagai K., Isogai T.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK123546; BAC85641.1; -.
 DR HSSP; P01842; IAOX.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; IGV; 4.
 DR SMART; SM00407; IGV; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 494 AA; 53321 MW; CD8140B37A23A882 CRC64;

Query Match 85.4%; Score 82; DB 2; Length 494;
 Best Local Similarity 82.4%; Pred. No. 0.00034;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINMGSTGYADSVKG 17
 Db 69 GIDMGDAGYADSVKG 85

RESULT 4
 Q9UL87 PRELIMINARY; PRT; 104 AA.
 ID Q9UL87
 AC Q9UL87
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
 RA Young D.C.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035027; AAD56263.1; -.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match 82.3%; Score 79; DB 2; Length 104;
 Best Local Similarity 82.4%; Pred. No. 0.0002;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINMGSTGYADSVKG 17
 Db 29 GISMGSTGYADSVKG 45

RESULT 5
 Q8WU38 PRELIMINARY; PRT; 573 AA.
 ID Q8WU38
 AC Q8WU38
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toohyuki S., Caraminci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
RA Krzywiński M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Straubeberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC021276; AAH21276.1; -.
DR PIR: S21205; S21205.
DR PIR: S30532; S30532.
DR HSSP: P18529; 118K.
DR Pfam: PF00047; 1g_1.
DR Pfam: PF00047; 1g_1.
DR SMART: SM00406; 1g_1.
DR PROSITE: PS50835; 1g_LIKE; 4.
DR PROSITE: PS00290; 1g_MHC; UNKNOWN_2.
DR Hypochemical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 82.3%; Score 79; DB 2; Length 573;
Best local Similarity 82.4%; Pred. NO. 0.0011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTYADSVKG 17
Db 69 GISMNGSIVYADSVKG 85

RESULT 6
ID 06N089 PRELIMINARY; PRT; 472 AA.
AC 06N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambut R., Heubner D., Mewes H.W., Well B., Amlid C., Osanger A.,
RA Fobio G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640627; CAE45781.1; -.
DR HSSP: P01861; 1ADQ.
DR InterPro: IPR003599; 1g.
DR InterPro: IPR007110; 1g_1like.
DR InterPro: IPR003597; 1g_1.

DR InterPro: IPR003006; 1g_MHC.
DR InterPro: IPR003596; 1g_V.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00409; 1g_2.
DR SMART: SM00407; 1g_1.
DR SMART: SM00406; 1g_1.
DR PROSITE: PS50835; 1g_LIKE; 4.
DR PROSITE: PS00290; 1g_MHC; UNKNOWN_2.
DR Hypochemical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 76.0%; Score 73; DB 2; Length 472;
Best local Similarity 76.5%; Pred. NO. 0.0081;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINWNGSGTYADSVKG 17
Db 69 GISMNGSIVYADSVKG 85

RESULT 7
ID HV3U_HUMAN STANDARD; PRT; 120 AA.
AC P01782;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 1g heavy chain V-III region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80020921; PubMed=114209;
RA Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT "Amino acid sequence of the heavy-chain variable region of the
crystallizable human myeloma protein Dob.";
RL Biochemistry 18:4068-4080(1979).
RN [2]
RP CRYSTALLIZATION.
RX MEDLINE=80020920; PubMed=114208;
RA Steiner L.A., Lopes A.D.;
RT "The crystallizable human myeloma protein Dob has a hinge-region
deletion.";
RL Biochemistry 18:4054-4067(1979).
CC -1- MISCELLANEOUS: This gamma-1 myeloma protein has a deletion in the
hinge region. There are no light-heavy or inter-heavy chain
disulfide bonds.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90431; GIH0DB.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; 1g_1like.
DR InterPro: IPR003596; 1g_V.
DR SMART: SM00407; 1g_1.
DR Pfam: PF00047; 1g_1.
DR PROSITE: PS50835; 1g_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 112
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 71.9%; Score 69; DB 1; Length 120;
Best local Similarity 81.2%; Pred. NO. 0.0083;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 INWNGSGTYADSVKG 17
Db 51 ITWNGSIVYADSVKG 66

DR PROSITE; PS50835;

Pfam: PF07654: C1-set: 4.

RESULT 12	ID	Q6DDQ7	PRELIMINARY;	PRT;	614 AA.
AC	Q6DDQ7	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)				
DE	MG669066 protein.				
GN	Name=MG669066;				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Spleen;				
RC	MEBLIN=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;				
RX	Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,				
RA	Richardson P.;				
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus				
RT	initiative."				
RL	Dev. Dyn. 225:384-391(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Spleen;				
RC	PubMed=12477932; DOI=10.1073/pnas.242603899;				
RX	Strusberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Klausner R.D., Collins E.A., Grouse L.H., Derge J.G.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan A., Moore T., Wax S.I., Wang J., Heien F.,				
RA	Datichenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Bromstein M.J., Udell T.B., Toshiyuki S., Caminici P., Prange C.,				
RA	Rata S.S., Lognani N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Boak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunnarone P.H.,				
RA	Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodegrem E.J., Lu X., Gibbs R.A.,				
RA	Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalela U., Smallus D.E., Schnerch A., Schein J.E.,				
RT	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Spleen;				
RC	Klein S., Strusberg R.;				
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, BC077477, AAH77477.1; --				
DR	InterPro: IPR003599; IG_				
DR	InterPro: IPR007110; IG_1like.				
DR	InterPro: IPR003597; IG_C1.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003596; IG_V.				
DR	InterPro: IPR001680; WD40.				
DR	Pfam; PF007654; Cl-sec; 4.				
DR	Pfam; PF00047; IG; 3.				

DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SQ SEQUENCE 614 AA; 68253 MW; 2631B7CF955270C0 CRC64;

Query Match 63.5%; Score 61; DB 2; Length 614;
Best Local Similarity 56.5%; Pred. No. 0.78;
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17
Db 61 GLOWSVISDGGSTYADSVKG 83

RESULT 13

ID O6INK3 PRELIMINARY; PRT; 584 AA.
AC O6INK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toehycki S., Carninci P., Prange C.T.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smallus D.E., Scherch A., Schein J.R.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Straube R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Klein S., Straube R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072277; AAH72277.1; --
DR HSSP; P01842; IAK.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sec; 2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KM Hypothetical protein.
SQ SEQUENCE 584 AA; 64449 MW; F1349DD169FD64 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 584;
Best Local Similarity 56.5%; Pred. No. 1.1;
Matches 13; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17
Db 63 GLOWSVISDGGSTYADSVKG 85

RESULT 14

ID HV53 MOUSE STANDARD; PRT; 117 AA.
AC HV53; P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=99279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR F01; J0503; HVMSRF.
DR HSSP; P18529; 118K.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hybridoma; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CB3295390F725B CRC64;

Query Match 61.5%; Score 59; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.29;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 INNWGSGTGYADSVKG 17
Db 70 INNSGSTYPTDVKG 85

RESULT 15
Q6GMX2 PRELIMINARY; PRT; 493 AA.

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AC O6GMX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueffing T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lottellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073771; AAH73771.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-set; 2.
DR Pfam: PF00047; IG; 3.
DR SMART: SM00409; IG; 4.
DR SMART: SM00407; IGcl; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG-LIKE; 4.
DR PROSITE: PSS0230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 55B999305B286203 CRC64;

Query Match 61.5%; Score 59; DB 2; Length 493;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 INNNGSGTGYADSVKG 17
| : | | | | | | | |
DB 70 INSDGSSTSYADSVKG 85

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Search completed: April 25, 2005, 20:34:03
 Job time : 9.78271 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 3.67849 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPVY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	AAW77197	AAW77197 Pharmaceu
2	29	100.0	6	ABG78133	Abg78133 Human Fv
3	29	100.0	6	ABG91824	Abg91824 Human ant
4	29	100.0	6	AD128369	Ad128369 Human CDR
5	29	100.0	6	ADJ57364	Adj57364 P-selecti
6	29	100.0	246	ABG78329	Abg78329 Human Fv
7	29	100.0	246	ABG92026	Abg92026 Antibody
8	29	100.0	256	ABG78334	Abg78334 Human Fv
9	29	100.0	256	ABG92025	Abg92025 Antibody
10	29	100.0	266	ABG92020	Abg92020 Human ant
11	29	100.0	277	ABG78150	Abg78150 Human Fv
12	29	100.0	277	ABG91841	Abg91841 Human ant
13	29	100.0	277	AD128366	Ad128366 Human scf
14	29	100.0	280	AD128367	Ad128367 Human scf
15	29	100.0	280	AD128368	Ad128368 Human scf
16	29	100.0	280	ADJ57363	Adj57363 P-selecti
17	29	100.0	442	ADN25218	Adn25218 Bacteri
18	29	100.0	464	ABG78151	Abg78151 Human Fv
19	29	100.0	464	ABG92021	Abg92021 Antibody
20	29	100.0	464	ABG91842	Abg91842 Human ant
21	28	96.6	133	AAU42688	Aau42688 Propionib
22	28	96.6	133	ABM39207	Abm39207 Propionib
23	28	96.6	438	AAE14569	Aae14569 Human rho
24	28	96.6	438	ADA13449	Ada13449 Human rho
25	28	96.6	438	ADA13415	Ada13415 Human rho

26	28	96.6	438	7	ADG47134	Adg47134 Human rho
27	28	96.6	438	7	ADG47100	Adg47100 Human rho
28	28	96.6	470	7	ADA13459	Ada13459 Mouse rho
29	28	96.6	541	7	ADG47144	Adg47144 Mouse rho
30	28	96.6	540	4	AAAG90242	Aag90242 C glutam
31	28	96.6	973	7	ABO75198	AbO75198 Pseudomon
32	27	93.1	116	4	AAU44808	Aau44808 Propionib
33	27	93.1	116	6	ABM41327	Abm41327 Propionib
34	26	89.7	33	4	AAAM82945	Aam82945 Human imm
35	26	89.7	33	4	AAU56719	Aau56719 Propionib
36	26	89.7	58	6	ABM53238	Abm53238 Propionib
37	26	89.7	226	5	ABP73581	Abp73581 Candida a
38	26	89.7	286	4	AAAG8915	Aag8915 E. coli g
39	26	89.7	286	6	ABU15292	Abu15292 Protein e
40	26	89.7	286	8	ADG45133	Adg45133 Bacteri
41	26	89.7	290	6	ABU28269	Abu28269 Protein e
42	26	89.7	350	2	AAV35225	Aav35225 Chlamydia
43	26	89.7	405	7	ADC87283	Adc87283 Human GPC
44	26	89.7	477	7	ABO62389	AbO62389 Klebsiell
45	26	89.7	1449	4	ABB66060	Abb66060 Drosophil

ALIGNMENTS

RESULT 1
AAW77197 standard; peptide; 6 AA.
ID AAW77197
AC AAW77197;
DT 23-NOV-1998 (first entry)
DE Pharmaceutically active peptide 38.
XX Pharmaceutically active peptide; target; organ; lymphocyte; treatment;
XX pharmaceutical agent; disease; radioactive isotope; imaging agent.
OS Synthetic.
OS Homo sapiens.
PN WO9839469-A1.
XX
PD 11-SEP-1998.
XX
PF 04-MAR-1998; 98WO-US004188.
XX
PR 04-MAR-1997; 97US-0039509P.
PR 04-MAR-1997; 97US-00810074.
XX
PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX Panel A, Hagai Y, Lazarovits J, Nimrod A, Vogel T, Levanon A;
PI Zeelon E, Belkind A, Golani I,
XX WPI, 1998-495863/42.
XX
XX New peptide(s) binding targets in organs and lymphocytes - used for the
PT targeted delivery of toxins, anti-cancer drugs and cardiovascular agents
PT to arteries, veins, placenta, liver.
XX
PS Claim 76; Page 99; 114pp; English.
XX
XX Sequences shown in AAW77160 to AAW77214 and AAW79167 represent non-
XX naturally-occurring pharmaceutically active peptides. These novel
XX peptides specifically bind to undetermined and determined targets in
XX various organs and in lymphocytes. The peptides can be used in
XX compositions, where they can be linked to pharmaceutical agents, to treat
XX various diseases and conditions. The peptides or chimeric polypeptides
XX comprising these pharmaceutically active peptides and a second peptide
XX may be labelled with a marker (radioactive isotope, etc) to form an
XX imaging agent. This agent is used to bind an organ so that the organ can
XX be imaged

XX Sequence 6 AA;
SQ

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
1 MRAPVI 6

RESULT 2
ABG78133
ID ABG78133 standard; peptide; 6 AA.

XX AC ABG78133;
XX DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #8.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cyrostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

XX MO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;

XX PI Plakain D, Peretz T;

XX DR WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.

XX Claim 2; Page 76; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has actively against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 3
ABG91824
ID ABG91824 standard; peptide; 6 AA.

XX AC ABG91824;
XX DT 04-DEC-2002 (first entry)

DE Human antibody fragment #8.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW revascularisation; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

XX MO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Max-Haim H;

XX PI Sanchon E, Richter T, Amit B, Koopman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.

XX Claim 1; Page 228; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRAPVI 6

RESULT 6
ABG78329

ID ABG78329 standard; protein; 246 AA.

AC ABG78329;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #204.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;

XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;

XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

XX MO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001MO-US049440.

XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;

XX Plaksin D, Peretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

XX PS Disclosure; Page 44-45; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv

XX molecule, a construct or fragments or a construct of a fragment with

XX enhanced binding characteristics which selectively and/or specifically

XX bind to a target cell in favour of other cells, where binding is

XX primarily determined by a first hypervariable region and Fv is a single

XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX association with or attached, coupled, combined, linked or fused to a

XX pharmaceutical agent, is useful in the manufacture of a medicament, where

XX the medicament has activity against a diseased cell, preferably a cancer

XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

XX acute myeloid leukaemia cell). The peptide is also useful for preparing a

XX composition for use in inhibiting the growth of a diseased or cancer

XX cell. This sequence represents a human Fv molecule hypervariable region

XX related peptide of the invention

XX Sequence 246 AA;

XX Query Match 100.0%; Score 29; DB 5; Length 246;

XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MRAPVI 6

XX 100 MRAPVI 105

RESULT 7
ABG92026

ID ABG92026 standard; protein; 246 AA.

AC ABG92026;

XX 04-DEC-2002 (first entry)

XX Antibody protein #5.

XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX metastasis; hypervariable region; autoimmune disease; thrombosis;

XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;

XX myocardial infarction; retinopathic disease; abnormal platelet function;

XX sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

XX MO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001MO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

XX Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in

XX physiological phenomena such as cell rolling, metastasis and

XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular

XX PT diseases, and cancer.

XX PS Disclosure; Fig 52; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and

XX important in physiological phenomena such as cell rolling, metastasis and

XX inflammation, where the epitope is capable of being bound by an antibody,

XX its antigen-binding fragment or its complex comprising at least one

XX antibody or its binding fragment having a first hypervariable region. The

XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

XX disease, thrombosis, restenosis, metastasis, growth and/or replication of

XX tumour or leukaemia cells, increase in number of tumour or leukaemia

XX cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

XX platelet and/or cell-platelet adhesion or aggregation, for increasing

XX mortality of tumour or leukaemia cells, for increasing the susceptibility

XX of diseased cells to damage by anti-disease, anti-cancer or anti-

XX leukaemia agents, or for decreasing the number of tumour or leukaemia

XX cells in a patient, or in the manufacture of a medicament for the above

XX mentioned purposes. The epitopes are useful for diagnosing and treating

XX diseases, cardiovascular diseases such as myocardial infarction,

XX retinopathic diseases and other diseases mediated by abnormal platelet

XX function and diseases caused by sulphated tyrosine-dependent protein-

XX protein interactions. This sequence represents an antibody protein of the

XX invention

XX Sequence 246 AA;

XX Query Match 100.0%; Score 29; DB 5; Length 246;

XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MRAPVI 6

XX 100 MRAPVI 105

RESULT 8
ABG78334

ID ABG78334 standard; protein; 256 AA.

AC

AC ABG78334;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #209.
 XX
 KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;
 XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 OS Homo sapiens.
 PN WO200253264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX
 DR WPI; 2002-619166/66.
 XX
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 PS Example 9; Page 90; 232pp; English.
 XX
 CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 CC
 SQ Sequence 256 AA;
 XX
 QY
 DB 100.0%; Score 29; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 100 MRAPVI 105
 RESULT 9
 ABG92025
 ID ABG92025 standard; protein; 256 AA.
 XX
 AC ABG92025;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Antibody biotag #1.
 XX
 KW Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;

KW restenosis; leukemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS unidentified.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure, Fig 51; 0pp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukemia agents, or for decreasing the number of tumour or leukemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody biotag used in
 CC the scope of the invention
 CC
 SQ Sequence 256 AA;
 XX
 QY
 DB 100.0%; Score 29; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 100 MRAPVI 105
 RESULT 10
 ABG92020
 ID ABG92020 standard; protein; 266 AA.
 XX
 AC ABG92020;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #204.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

XX 11-JUL-2002.

PD 31-DEC-2001; 2001WO-US049442.

PF 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 DR MPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

PS Disclosure; Page 309-310; Opp; English.

CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

SO Sequence 266 AA;

Query Match 100.0%; Score 29; DB 5; Length 266;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6

DB 121 MRAPI 126

RESULT 11

ABG78150 standard; protein; 277 AA.

XX ABG78150;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

KM Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

PN WO200259264-A2.

XX 01-AUG-2002.

PD 31-DEC-2001; 2001WO-US049440.

PF 29-DEC-2000; 2000US-00751181.

PR (BIOT-) BIO-TECHNOLOGY GEN CORP.

PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 DR MPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

PS Claim 4; Page 155-156; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

SO Sequence 277 AA;

Query Match 100.0%; Score 29; DB 5; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6

DB 121 MRAPI 126

RESULT 12

ABG91841 standard; protein; 277 AA.

XX ABG91841;

DT 04-DEC-2002 (first entry)

DE Human antibody fragment #25.

KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanboun E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Claim 23; Page 233-234; Opp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 CC
 SQ Sequence 277 AA;
 XX
 Query Match 100.0%; Score 29; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPIV 6
 DB 121 MRAPIV 126
 XX
 RESULT 13
 ADI28366 standard; protein; 277 AA.
 XX
 AC ADI28366;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment Y1, binds to platelets.
 XX
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 PD 08-JAN-2004.
 XX

XX
 XX 30-JUN-2003; 2003WO-US020604.
 XX
 PF 01-JUL-2002; 2002US-00189025.
 XX
 PR (SAVI-) SAVIENT PHARM INC.
 XX
 PA Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 PI WPI; 2004-099189/10.
 XX
 DR
 XX
 PT Composition comprising an agent and/or antibody or its fragment, useful
 PT for treating autoimmune disease, thrombosis, restenosis, metastasis, or
 PT for inhibiting growth and/or replication of tumor cells or leukemia
 PT cells.
 XX
 PS Claim 13; SEQ ID NO 1; 58pp; English.
 XX
 CC The present sequence is the protein sequence of human scFv fragment Y1.
 CC This antibody was identified by screening a human antibody phage library
 CC that has diversity only in the heavy chain CDR3 regions. Fixed human
 CC platelets were screened in order to identify antibodies that bind
 CC platelets. The epitope for Y1 antibody is located between amino acids 272
 CC and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the
 CC N-terminal of PSGL-1, a receptor for E-, L- and P-selectins, and has a
 CC high affinity for primary leukaemia cells. The invention relates to
 CC compositions utilising an agent and an antibody or its fragment. The
 CC agent is a toxin, radioisotope or pharmaceutical agent such as
 CC doxorubicin. It is complexed or combined with or conjugated to the
 CC antibody or its fragment. The agent and/or antibody can be present in the
 CC composition as a sub-clinical amount, i.e. less than the amount generally
 CC found to be clinically effective when the agent is administered alone.
 CC The composition is used in claimed methods of: inhibiting cell rolling,
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
 CC replication of tumour cells or leukaemia cells, an increase in number of
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
 CC susceptibility of disease cells to damage by anti-disease agents, and the
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
 CC agents; and ameliorating the effects of a disease, preventing a disease,
 CC treating a disease or inhibiting the progress of a disease.
 CC
 SQ Sequence 277 AA;
 XX
 Query Match 100.0%; Score 29; DB 8; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPIV 6
 DB 121 MRAPIV 126
 XX
 RESULT 14
 ADI28367 standard; protein; 278 AA.
 XX
 AC ADI28367;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment Y17, binds to platelets.
 XX
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020604.
 XX

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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 0.924612 Seconds
(without alignments)
484.413 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPVI 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

513545

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	96.6	973	4 US-09-252-991A-23944	Sequence 23944, A
2	26	89.7	229	4 US-09-248-796A-16460	Sequence 16460, A
3	26	89.7	286	4 US-09-711-164-385	Sequence 385, App
4	26	89.7	350	4 US-09-198-452A-643	Sequence 643, App
5	26	89.7	350	4 US-09-438-185A-605	Sequence 605, App
6	26	89.7	477	4 US-09-489-039A-8906	Sequence 8906, App
7	25	86.2	119	4 US-09-252-991A-28425	Sequence 28425, A
8	25	86.2	130	4 US-09-107-532A-6688	Sequence 6688, App
9	25	86.2	197	4 US-09-902-540-13013	Sequence 13013, A
10	25	86.2	222	4 US-09-489-039A-8244	Sequence 8244, App
11	25	86.2	222	4 US-09-538-092-272	Sequence 272, App
12	25	86.2	223	4 US-09-134-000C-6010	Sequence 6010, App
13	25	86.2	224	4 US-09-538-092-617	Sequence 617, App
14	25	86.2	233	4 US-09-489-039A-7366	Sequence 7366, App
15	25	86.2	239	4 US-09-328-352-5866	Sequence 5866, App
16	25	86.2	291	4 US-09-602-777A-36	Sequence 36, App1
17	25	86.2	359	4 US-09-252-991A-19964	Sequence 19964, A
18	25	86.2	417	4 US-09-270-767-44567	Sequence 44567, A
19	25	86.2	481	4 US-09-252-991A-26783	Sequence 26783, A
20	25	86.2	481	4 US-09-489-039A-10515	Sequence 10515, A
21	25	86.2	487	4 US-09-583-110-3569	Sequence 3569, App
22	25	86.2	488	4 US-09-107-433-3552	Sequence 3552, App
23	25	86.2	657	4 US-09-252-991A-27682	Sequence 27682, App
24	25	86.2	885	4 US-09-902-540-13431	Sequence 13431, A
25	25	86.2	962	4 US-09-328-352-7942	Sequence 7942, App
26	24	82.8	73	4 US-09-621-976-6392	Sequence 6392, App
27	24	82.8	76	4 US-09-636-215-575	Sequence 575, App

28	24	82.8	76	4	US-09-685-166A-575	Sequence 575, App
29	24	82.8	76	4	US-09-685-166A-888	Sequence 888, App
30	24	82.8	76	4	US-09-679-426-575	Sequence 575, App
31	24	82.8	76	4	US-09-679-426-888	Sequence 888, App
32	24	82.8	76	4	US-09-759-143-575	Sequence 575, App
33	24	82.8	76	4	US-09-759-143-888	Sequence 888, App
34	24	82.8	76	4	US-09-651-736-575	Sequence 575, App
35	24	82.8	89	3	US-09-134-001C-4676	Sequence 4676, App
36	24	82.8	93	4	US-09-134-001C-4563	Sequence 4563, App
37	24	82.8	93	4	US-09-938-806A-8	Sequence 8, App1
38	24	82.8	102	4	US-09-248-796A-14433	Sequence 14433, A
39	24	82.8	108	4	US-09-513-999C-5944	Sequence 5944, App
40	24	82.8	125	3	US-09-199-637A-403	Sequence 403, App
41	24	82.8	125	4	US-09-269-410-11	Sequence 11, App1
42	24	82.8	125	4	US-09-513-999C-5838	Sequence 5838, App
43	24	82.8	143	4	US-09-270-767-42631	Sequence 42631, A
44	24	82.8	152	3	US-08-801-742-3	Sequence 3, App1
45	24	82.8	192	1	US-08-208-008C-9	Sequence 9, App1

ALIGNMENTS

```
RESULT 1
US-09-252-991A-23944
; Sequence 23944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23944
; LENGTH: 973
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23944

Query Match          96.6%; Score 28; DB 4; Length 973;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 MRAPVI 6
Db      387 MRAPV 392

RESULT 2
US-09-248-796A-16460
; Sequence 16460, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16460
; LENGTH: 229
; TYPE: PRT
```

; ORGANISM: Candida albicans
US-09-248-796A-16460

Query Match 89.7%; Score 26; DB 4; Length 229;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
|:||||
Db 182 MKAPI 187

RESULT 3

US-09-711-164-385
; Sequence 385, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Olsen, Karl
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711.164
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-711-164-385

Query Match 89.7%; Score 26; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
|:||||
Db 41 MRAPI 46

RESULT 4

US-09-198-452A-643
; Sequence 643, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198.452A
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 643
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-643

Query Match 89.7%; Score 26; DB 4; Length 350;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
|:||||
Db 109 MRAPI 114

RESULT 5
US-09-438-185A-605

; Sequence 605, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438.185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108.279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128.606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 605
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0603
US-09-438-185A-605

Query Match 89.7%; Score 26; DB 4; Length 350;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
|:||||
Db 109 MRAPI 114

RESULT 6

US-09-489-039A-8906
; Sequence 8906, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117.747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8906
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8906

Query Match 89.7%; Score 26; DB 4; Length 477;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
|:||||
Db 269 MRAPI 274

RESULT 7

US-09-252-991A-28425
; Sequence 28425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 28425
;; LENGTH: 119
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28425

Query Match 86.2%; Score 25; DB 4; Length 119;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPI 6
Db 63 MRAPI 68

RESULT 8
US-09-107-532A-6688
; Sequence 6688, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6688:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...120

SEQUENCE DESCRIPTION: SEQ ID NO: 6688:

US-09-107-532A-6688

Query Match 86.2%; Score 25; DB 4; Length 120;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
Db 17 MRAPI 22

RESULT 9
US-09-902-540-13013
; Sequence 13013, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13013
LENGTH: 197
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-13013

Query Match 86.2%; Score 25; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 5
Db 1 MRAPI 5

RESULT 10
US-09-489-039A-8244
; Sequence 8244, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8244
LENGTH: 222
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8244

Query Match 86.2%; Score 25; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 5
Db 24 MRAPI 28

RESULT 11
US-09-538-092-272
; Sequence 272, Application US/09538092
; Patent No. 6753314

```

; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO: 272
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YFL060C
US-09-538-092-272
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Query Match      86.2%; Score 25; DB 4; Length 222;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MRAPV 6
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Db       151 IRAPV 156
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RESULT 12
; Sequence 6010, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6010
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6010
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Query Match      86.2%; Score 25; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MRAPV 5
        :|||||
Db       127 MRAPV 131
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```

RESULT 13
US-09-538-092-617
; Sequence 617, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
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; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO: 617
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YMR095C
US-09-538-092-617
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Query Match      86.2%; Score 25; DB 4; Length 224;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MRAPV 6
        :|||||
Db       160 IRAPV 165
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RESULT 14
US-09-489-039A-7366
; Sequence 7366, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO: 7366
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7366
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Query Match      86.2%; Score 25; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MRAPV 5
        :|||||
Db       173 MRAPV 177
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RESULT 15
US-09-328-352-5866
; Sequence 5866, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO: 5866
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5866
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Query Match      86.2%; Score 25; DB 4; Length 239;
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Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
|:|:|:
Db 140 MKAPVV 145

Search completed: April 25, 2005, 21:12:11
Job time : 1.92461 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 2.6541 Seconds
(without alignments)
752.325 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29
Sequence: 1 MRAPIV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubppa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	US-10-032-037B-8	Sequence 8, Appli
2	29	100.0	6	US-10-029-988B-8	Sequence 8, Appli
3	29	100.0	6	US-10-032-423A-8	Sequence 8, Appli
4	29	100.0	6	US-10-029-926B-8	Sequence 8, Appli
5	29	100.0	6	US-10-880-922-4	Sequence 4, Appli
6	29	100.0	266	US-10-032-037B-204	Sequence 204, App
7	29	100.0	266	US-10-029-988B-204	Sequence 204, App
8	29	100.0	266	US-10-032-423A-204	Sequence 204, App
9	29	100.0	277	US-10-032-037B-25	Sequence 25, Appl
10	29	100.0	277	US-10-029-988B-25	Sequence 25, Appl
11	29	100.0	277	US-10-032-423A-25	Sequence 25, Appl
12	29	100.0	277	US-10-029-926B-25	Sequence 25, Appl
13	29	100.0	442	US-10-369-493-7871	Sequence 7871, Ap

14	29	100.0	464	US-10-032-037B-26	Sequence 26, Appl
15	29	100.0	464	US-10-029-988B-26	Sequence 26, Appl
16	29	100.0	464	US-10-032-423A-26	Sequence 26, Appl
17	29	100.0	464	US-10-029-926B-26	Sequence 26, Appl
18	29	100.0	86	US-10-424-559-253048	Sequence 253048,
19	28	96.6	123	US-10-424-559-150638	Sequence 150638,
20	28	96.6	438	US-09-908-419-2	Sequence 2, Appli
21	28	96.6	438	US-10-056-790-2	Sequence 2, Appli
22	28	96.6	438	US-10-056-790-36	Sequence 36, Appli
23	28	96.6	470	US-10-056-790-46	Sequence 46, Appli
24	28	96.6	541	US-09-738-626-3996	Sequence 3996, Ap
25	27	93.1	99	US-10-424-559-272558	Sequence 272558,
26	27	89.7	112	US-10-767-701-42410	Sequence 42410, A
27	26	89.7	226	US-10-032-585-7418	Sequence 7418, Ap
28	26	89.7	286	US-10-287-274-385	Sequence 385, App
29	26	89.7	286	US-10-369-493-23563	Sequence 23563, A
30	26	89.7	286	US-10-282-122A-43216	Sequence 43216, A
31	26	89.7	289	US-10-425-114-69148	Sequence 69148, A
32	26	89.7	290	US-10-282-122A-56193	Sequence 56193, A
33	26	89.7	319	US-10-425-114-55531	Sequence 55531, A
34	26	89.7	345	US-10-767-701-45307	Sequence 45307, A
35	26	89.7	350	US-10-289-762-643	Sequence 643, App
36	26	89.7	405	US-10-017-161-2090	Sequence 2090, Ap
37	26	89.7	405	US-10-292-795-1736	Sequence 1736, Ap
38	26	89.7	514	US-10-425-114-53835	Sequence 53835, A
39	26	89.7	530	US-10-425-114-60637	Sequence 60637, A
40	26	89.7	1428	US-10-437-963-144989	Sequence 144989,
41	25	86.2	58	US-10-437-963-177085	Sequence 1377085,
42	25	86.2	73	US-10-767-701-48548	Sequence 48548, A
43	25	86.2	75	US-10-424-559-196866	Sequence 196866,
44	25	86.2	104	US-10-437-963-164399	Sequence 164399,
45	25	86.2	110	US-10-437-963-158848	Sequence 158848,

ALIGNMENTS

RESULT 1
US-10-032-037B-8
; Sequence 8, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-8

Query Match 100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6
|||||
Db 1 MRAPIV 6

RESULT 2
US-10-029-988B-8
; Sequence 8, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.

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; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-029-988B-8

Query Match          100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
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Db       1 MRAPVI 6

RESULT 3
; US-10-032-423A-8
; Sequence 8, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-423A-8

Query Match          100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
        |||||
Db       1 MRAPVI 6

RESULT 4
; US-10-029-926B-8
; Sequence 8, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-029-926B-8
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Query Match          100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
        |||||
Db       1 MRAPVI 6

RESULT 5
; US-10-880-922-4
; Sequence 4, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANNON, DANIEL
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHAVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YAEI
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-880-922-4

Query Match          100.0%; Score 29; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
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Db       1 MRAPVI 6

RESULT 6
; US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-037B-204

Query Match          100.0%; Score 29; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRAPI 6
| | | | |
Db 121 MRAPI 126

RESULT 7

US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 100.0%; Score 29; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
| | | | |
Db 121 MRAPI 126

RESULT 8

US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match 100.0%; Score 29; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
| | | | |
Db 121 MRAPI 126

RESULT 9

US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
| | | | |
Db 121 MRAPI 126

RESULT 10
US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
| | | | |
Db 121 MRAPI 126

RESULT 11
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
121 MRAPI 126

RESULT 12

US-10-029-926B-25
; Sequence 25; Application US/10029926B
; Publication No. US2004073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
121 MRAPI 126

RESULT 13

US-10-369-493-7871
; Sequence 7871; Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7871
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7871

Query Match 100.0%; Score 29; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
77 MRAPI 82

RESULT 14
US-10-032-037B-26

; Sequence 26; Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-26

Query Match 100.0%; Score 29; DB 15; Length 464;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
118 MRAPI 123

RESULT 15

US-10-029-988B-26
; Sequence 26; Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-26

Query Match 100.0%; Score 29; DB 15; Length 464;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
118 MRAPI 123

Search completed: April 25, 2005, 21:09:47
Job time : 3.6541 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 0.691796 Seconds

(without alignments)
834.495 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPIV 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	249	2	H87675 hydrolyase, alpha/b
2	29	100.0	442	2	JC4733 Probable H+-transp
3	29	100.0	629	2	T37255 acetylcholinestera
4	28	96.6	425	2	S33045 hypothetical prote
5	27	93.1	247	2	H69030 coenzyme PQQ synth
6	26	89.7	286	2	A91131 tagatose-1,6-bisph
7	26	89.7	286	2	A85976 tagatose-bisphosph
8	26	89.7	286	2	E65103 ferriochelataase CP0
9	26	89.7	327	2	E72057 ferriochelataase [im
10	26	89.7	327	2	H86565 pmba protein - Esc
11	26	89.7	450	1	S13730 probable pmba prot
12	26	89.7	450	2	AE1056 maturation of anti
13	26	89.7	450	2	D86121 maturation of anti
14	26	89.7	450	2	D91280 maturation of anti
15	25	86.2	138	2	T24916 hypothetical prote
16	25	86.2	147	2	C95907 probable protein 1
17	25	86.2	147	2	F95924 hypothetical prote
18	25	86.2	149	2	C72419 conserved hypotet
19	25	86.2	144	2	A82812 conserved hypotet
20	25	86.2	163	2	A87412 hypothetical prote
21	25	86.2	195	2	F75399 antibiolic resista
22	25	86.2	196	2	G75405 probable amidoran
23	25	86.2	203	2	C84409 imidazoleglycerol-
24	25	86.2	232	2	S63320 imidazole membrane
25	25	86.2	222	2	S56195 probable membrane
26	25	86.2	224	2	S55081 hypothetical prote
27	25	86.2	227	2	C53304 transfer protein C
28	25	86.2	240	2	E69004 hypothetical prote
29	25	86.2	252	2	A88508 protein H14A12.4 (

30	25	86.2	261	2	AC3507 hief protein (impo
31	25	86.2	266	2	AC2407 tryptophan synthas
32	25	86.2	284	2	AF1341 fructose-1,6-bispho
33	25	86.2	284	2	AD1712 fructose-1,6-bispho
34	25	86.2	328	2	G96024 conserved hypotet
35	25	86.2	332	2	C81285 glyceraldehyde 3-P
36	25	86.2	359	2	A10112 fructose-bisphosph
37	25	86.2	362	2	F90200 hypothetical prote
38	25	86.2	398	2	B70752 hypothetical prote
39	25	86.2	422	2	AE3394 lipoprotein releas
40	25	86.2	422	2	E83083 probable two-compo
41	25	86.2	430	2	T16715 hypothetical prote
42	25	86.2	446	2	A84940 pmba protein (impo
43	25	86.2	463	2	AC0977 L-beeryl-tRNAseec se
44	25	86.2	487	2	T27353 hypothetical prote
45	25	86.2	489	2	JC4787 shaw protein - Cal

ALIGNMENTS

RESULT 1

H87675 hydrolyase, alpha/beta hydrolyase fold family [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #ext_change 12-Jul-2004
C/Accession: H87675

R/Nierman, W.C.; Feildblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gattim, M.L.; Hatt, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; NCBI:21173698; PMID:11259647

A/Accession: H87675

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <STO>

A/Cross-references: UNIPROT:Q9A2W4; GB:AE005673; NID:g13425158; PIDN:AAK25404.1; GSPDB:4

C/Genetics:

A/Gene: CC3442

C/Superfamily: tropinesterase

Query Match Best Local Similarity 100.0%; Score 29; DB 2; Length 249;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6
|||||
Db 1 MRAPIV 6

RESULT 2

JC4733 probable H+-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific - Rhodospirillum rubrum

C/Species: Rhodospirillum rubrum

C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #ext_change 09-Jul-2004

C/Accession: JC4733

R/Bellido, T.; Campos, A.; Camarena, L.; Dreyfus, G.

Gene 170, 69-72, 1996

A/Title: Flagellar genes from Rhodospirillum rubrum are homologous to genes of the fl

A/Reference number: JC4733; NCBI:96200857; PMID:8621091

A/Accession: JC4733

A/Molecule type: DNA

A/Residues: 1-442 <BAL>

A/Cross-references: UNIPROT:Q53093; GB:U31090; NID:g1518877; PIDN:AA07344.1; PID:g1293

C/Genetics:

A/Gene: flII

C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase a

C/Keyword: ATP; flagellum; hydrolyase; nucleotide binding; P-loop

F/168-175/Region: nucleotide-binding motif A (P-loop)

F/191-362/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

F/191-207/Region: ATP-binding #status predicted

F/242-258/Domain: beta chain #status predicted <BET>

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
| | | | |
Db 77 MRAPVI 82

RESULT 3

T37255
acetylcholinesterase (EC 3.1.1.7) 2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37255
R/Grauso, M.; Chiletto, E.; Combes, D.; Fedon, Y.; Toutant, J.P.; Arpagaus, M.
FEBS Lett. 424, 279-284, 1998
A/Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabditis el
A/Reference number: Z21648; MUID:98198570; PMID:9539167
A/Accession: T37255
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-629 <GRA>
A/Cross-references: UNIPROT:O61371; EMBL:AF025378; NID:95148937; PIDN:AAC14016.2; PID:95
A/Experimental source: strain N2
C/Genetics:
A/Map position: I
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase

Query Match 100.0%; Score 29; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
| | | | |
Db 1 MRAPVI 6

RESULT 4

S33045
hypothetical protein - human herpesvirus 4
C/Species: human herpesvirus 4, Epstein-Barr virus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33045
R/Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A/Reference number: S32973
A/Accession: S33045
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-425 <FAR>
A/Cross-references: UNIPROT:P30119; EMBL:V01555; NID:959074; PIDN:CAA24796.1; PID:913349
C/Superfamily: equine herpesvirus 2 hypothetical protein 23

Query Match 96.6%; Score 28; DB 2; Length 425;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
| | | | |
Db 87 MRAPVI 92

RESULT 5

H69030
coenzyme PQQ synthesis protein III - Methanobacterium thermoautotrophicum (strain Delta
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: H69030
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A/Reference number: A69000; MUID:98037514; PMID:9371463

A/Accession: H69030
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-247 <MTH>
A/Cross-references: UNIPROT:Q27295; GB:AE000890; GB:AE000666; NID:92622311; PIDN:AAB8571
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH1227
A/Start codon: GTG
C/Keywords: iron; metalloprotein
F/34,38,41/Binding site: iron (Cys) #status predicted

Query Match 93.1%; Score 27; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
| | | | |
Db 4 MRAPVI 9

RESULT 6

A91131
tagatose-1,6-bisphosphate aldolase [imported] - Escherichia coli (strain O157:H7, substra
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A91131
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: A91131
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-266 <HAY>
A/Cross-references: UNIPROT:P42908; GB:BA000007; PIDN:BA837440.1; PID:913363490; GSPDB:
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: EC64017
C/Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
| | | | |
Db 41 MRAPVI 46

RESULT 7

A85976
tagatose-bisphosphate aldolase 2 [imported] - Escherichia coli (strain O157:H7, substra
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: A85976
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; DiMantana, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85976
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1286 <STO>
A/Cross-references: UNIPROT:P42908; GB:AE005174; NID:912517735; PIDN:AAG58269.1; GSPDB:
A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:
A/Genes: agay
C/Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 41 MRSPVI 46

RESULT 8

B65103
ferrochelatase aldolase agay (EC 4.1.2.-) - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: B65103
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; PMID:97426617; PMID:9278503
A/Accession: B65103
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <BLAT>
A/Cross-references: UNIPROT:P42908; GB:AE000395; GB:U00096; NID:g1789524; PIDN:AACT6171.
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Genes: agay
C/Superfamily: fructose-bisphosphate aldolase II
C/Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 41 MRSPVI 46

RESULT 9

E72057
ferrochelatase CP0144 [imported] - Chlamydia pneumoniae (strains CML029 and AR39)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: E72057; F81609
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; PMID:99206606; PMID:10192388
A/Accession: E72057
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-327 <ARN>
A/Cross-references: UNIPROT:Q927V1; GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AMD1874
A/Experimental source: strain CML029
R/Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gilm, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoDn and Chlamydia pneumoniae AR39.
A/Reference number: AB1500; PMID:20150255; PMID:10684935
A/Accession: F81609
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-327 <RBA>
A/Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AAF38026.1; PID:g718907
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Genes: hemz; CP0144

C/Superfamily: ferrochelatase

Query Match 89.7%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 86 LRAPVI 91

RESULT 10

H86565
ferrochelatase [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H86565
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; PMID:20330349; PMID:10873362
A/Accession: H86565
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-327 <STO>
A/Cross-references: UNIPROT:Q927V1; GB:BA000008; NID:g8978975; PIDN:BA098810.1; GSPDB:G
A/Experimental source: strain J138
C/Genetics:
A/Genes: hemz

Query Match 89.7%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 86 LRAPVI 91

RESULT 11

S13730
pmba protein - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 09-Jul-2004
C/Accession: S13730; S56461; F65235
R/Rodriguez-Sainz, M.C.; Hernandez-Chico, C.; Moreno, F.
Mol. Microbiol. 4, 1921-1932, 1990
A/Title: Molecular characterization of pmbA, an Escherichia coli chromosomal gene requi
A/Reference number: S13730; PMID:91186828; PMID:2082149
A/Accession: S13730
A/Molecule type: DNA
A/Residues: 1-450 <ROD>
A/Cross-references: UNIPROT:P24231; EMBL:X54152; NID:g42439; PIDN:CAA8091.1; PID:g42444
R/Burland, V.; Plunkett III, G.; Sofia, H.D.; Daniele, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A/Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92
A/Reference number: S56314; PMID:95334362; PMID:7610040
A/Accession: S56461
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-450 <BUR>
A/Cross-references: EMBL:U14003; NID:g1263172; PIDN:AA97132.1; PID:g537077
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; PMID:97426617; PMID:9278503
A/Accession: F65235
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-450 <BLAT>
A/Cross-references: GB:AE000494; GB:U00096; NID:g1790670; PIDN:AACT7192.1; PID:g1790682

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 3.09978 Seconds

(without alignments)
991.192 Million cell updates/sec

Title: US-10-029-926D-8

Sequence: 1 MRAPV1 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	249	2 Q9A2M4	Q9A2M4 caulobacter
2	29	100.0	309	2 Q63ZV1	Q63ZV1 mus musculu
3	29	100.0	442	2 Q53093	Q53093 rhodobacter
4	29	100.0	442	2 Q53153	Q53153 rhodobacter
5	29	100.0	629	2 Q61371	Q61371 caenorhabdi
6	29	100.0	939	2 Q6PD31	Q6PD31 mus musculu
7	29	100.0	947	2 Q80T16	Q80T16 mus musculu
8	28	96.6	164	1 RBH1_PAT	RBH1_PAT
9	28	96.6	231	2 Q6PD44	Q6PD44 acinetobact
10	28	96.6	373	1 RBH1_MOUSE	RBH1_MOUSE
11	28	96.6	376	2 Q8P9F5	Q8P9F5 mus musculu
12	28	96.6	425	1 YTR1_EBV	YTR1_EBV
13	28	96.6	425	2 Q777C1	Q777C1 human herpe
14	28	96.6	438	1 RBH1_HUMAN	RBH1_HUMAN
15	28	96.6	541	2 Q8NT69	Q8NT69 corynebacte
16	28	96.6	577	2 Q6CTG6	Q6CTG6 kluyveromyc
17	28	96.6	713	2 Q7YVY3	Q7YVY3 cryptospori
18	27	93.1	247	2 Q27295	Q27295 methanobact
19	27	93.1	376	2 Q9L778	Q9L778 xanthomonas
20	27	93.1	376	2 Q8PL69	Q8PL69 xanthomonas
21	27	93.1	416	2 Q9AC09	Q9AC09 streptomyce
22	27	93.1	449	2 Q89X81	Q89X81 bradyrhizob
23	27	93.1	535	1 TLE1_BRAE	TLE1_BRAE
24	27	93.1	771	2 Q98TH2	Q98TH2 brachydania
25	26	89.7	162	2 Q8ILB7	Q8ILB7 plasmodium
26	26	89.7	162	2 Q7RL13	Q7RL13 plasmodium
27	26	89.7	199	2 Q6BSE3	Q6BSE3 debaromyce
28	26	89.7	250	1 PDX0_BRAJA	PDX0_BRAJA
29	26	89.7	264	1 Q7F2A7	Q7F2A7 oryza sativ
30	26	89.7	286	1 AGAY_ECOLI	AGAY_ECOLI
31	26	89.7	286	2 Q9K1F8	Q9K1F8 escherichia

32	26	89.7	305	2 Q65M26	Q65M26 bacillus li
33	26	89.7	327	1 HEM2_CHLUPN	HEM2_CHLUPN
34	26	89.7	353	2 Q9TE68	Q9TE68 nitazochia f
35	26	89.7	353	2 Q9TE71	Q9TE71 cylindrothe
36	26	89.7	450	1 PMBA_ECOLI	PMBA_ECOLI
37	26	89.7	450	2 Q8XGJ7	Q8XGJ7 salmonella
38	26	89.7	450	2 Q7CP84	Q7CP84 salmonella
39	26	89.7	450	2 Q7UNM7	Q7UNM7 shigella fl
40	26	89.7	450	2 Q83P54	Q83P54 shigella fl
41	26	89.7	450	2 Q8PAP2	Q8PAP2 escherichia
42	26	89.7	453	2 Q7UKY8	Q7UKY8 rhodospirill
43	26	89.7	535	2 Q8ER88	Q8ER88 oceanobacill
44	26	89.7	583	2 Q9VKE5	Q9VKE5 drosophila
45	26	89.7	1042	2 Q7QXR0	Q7QXR0 giardia lam

ALIGNMENTS

RESULT 1					
ID	Q9A2M4	PRELIMINARY;	PRT;	249 AA.	
AC	Q9A2M4;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Hydrolase, alpha/beta hydrolase fold family.				
GN	OrderedLocustNames=CC3442;				
OS	Caulobacter crescentus.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;				
OC	Caulobacteraceae; Caulobacter.				
NC	NCBI_TaxID=155892;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 19089 / CB15;				
RX	MEDLINE=21173698; PubMed=1259647; DOI=10.1073/pnas.061029298;				
RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.B.,				
RA	Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,				
RA	Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,				
RA	DeBoy R.T., Dodson R.C., Durkin A.S., Gwinn M.L., Shetty J.,				
RA	Kolman J.F., Smit J., Craven M.B., Knout H.M., Shetty J.,				
RA	Berry K.J., Uteirack T.R., Tran K., Wolf A.M., Vamathavan J.J.,				
RA	Ermoiaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,				
RA	Fraser C.M.;				
RT	"Complete genome sequence of Caulobacter crescentus.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).				
DR	EMBL; AB006003; AAK25404.1; -				
DR	PIR; H87675; H87675.				
DR	TIGR; CC3442; -				
DR	GO; GO:0016787; F:hydrolase activity; IEA.				
DR	GO; GO:006725; P:aromatic compound metabolism; IEA.				
DR	InterPro; IPR000073; A/B_hydrolase.				
DR	InterPro; IPR003089; AB_hydrolase.				
DR	InterPro; IPR000379; Ser_esterase.				
DR	Pfam; PF00561; ABhydrolase.1; 1.				
DR	PRINTS; PR00111; ABHYDROLASE.				
KW	Complete proteome; Hydrolase.				
SQ	SEQUENCE 249 AA; 26772 MW; 491350127DD300AE CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 29; DB 2; Length 249;					
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 MRAPV1 6				
Db	1 MRAPV1 6				
RESULT 2					
ID	Q63ZV1	PRELIMINARY;	PRT;	309 AA.	
AC	Q63ZV1;				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				

DT 25-OCT-2004 (TREMblrel. 28, last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, last annotation update)
 DE Hypothetical protein (Fragment).
 OC Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCB1_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
 RA Datchenko L., Mausina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RA Director MGC Project;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC082807; AA82807.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 309 AA; 32959 MW; 5F551A9B90CC8714 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPIV 6
 DB 286 MRAPIV 291

RESULT 3
 Q53093 PRELIMINARY; PRT; 442 AA.
 AC Q53093;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Flii.
 GN Flii;
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 ON NCB1_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2.4.1;
 RX MEDLINE=96200857; PubMed=8621091; DOI=10.1016/0378-1119(95)00855-1;
 RA Ballado T., Campos A., Camarena L., Dreyfus G.;
 RT "Flaegellar genes from Rhodobacter sphaeroides are homologous to genes
 of the flif operon of Salmonella typhimurium and to the type-III
 secretion system.";
 RL Gene 170:69-72(1996).
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

DR EMBL; U31090; AA807344.1; -.
 DR PIR; JC4733; JC4733.
 DR HSSP; P03002; LPVO.
 DR GO; GO:0005737; C:Cytoplasm; IEA.
 DR GO; GO:001469; C:proton-transporting two-sector ATPase complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
 DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.
 DR GO; GO:0016787; F:hydroxylase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0015986; F:ATP synthase coupled proton transport; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR InterPro; IPR004100; ATPase_a/b_N.
 DR InterPro; IPR005714; Flii_YscN.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRfams; TIGR01026; Flii_YscN; 1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 KW ATP synthase; ATP-binding; Hydroxylase; ion transport; Transport.
 SQ SEQUENCE 442 AA; 46852 MW; E6D35531F5A59BAE CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1,2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPIV 6
 DB 77 MRAPIV 82

RESULT 4
 Q53153 PRELIMINARY; PRT; 442 AA.
 AC Q53153;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Flii protein.
 GN Flii;
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 ON NCB1_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WS8;
 RX MEDLINE=96377148; PubMed=8759796; DOI=10.1016/0378-1097(96)00252-2;
 RA Goodfellow I.G., Pollitt C.E., Sockett R.E.;
 RT "Cloning of the flii gene from Rhodobacter sphaeroides WS8 by analysis
 of a transposon mutant with impaired motility.";
 RL FEMS Microbiol. Lett. 142:111-116(1996).
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
 DR EMBL; X97201; CA65834.1; -.
 DR HSSP; P03002; LPVO.
 DR GO; GO:0005737; C:Cytoplasm; IEA.
 DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
 DR GO; GO:0016787; F:hydroxylase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0015986; F:ATP synthase coupled proton transport; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000194; ATPase_a/bcentre.

DR InterPro: IPR004100; ATPase_a/b_N.
 DR InterPro: IPR005714; F111_YECN.
 DR Pfam: PF00006; ATP-8ynt_ab; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRfam: TIGR01026; f111_yecN; 1.
 DR PROSITE: PS00152; ATPase_ALPHA_BETA; UNKNOWN 1.
 DR ATP synthetase; ATP-binding; Hydrolase; Ion transport; Transport.
 KW SEQUENCE 442 AA; 46813 MW; AD070D4B17FD3CC3 CRC64;
 SQ

Query Match 100.0%; Score 29; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 77 MRAPVI 82

RESULT 5
 061371 PRELIMINARY; PRT; 629 AA.
 AC 061371; O9TKY7;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Acetylcholinesterase (EC 3.1.1.7) (Abnormal acetylcholinesterase protein 2).
 GN Name: ace-2; ORFNames=Y44E3A.2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RA MEDLINE=98198570; PubMed=9539167; DOI=10.1016/S0014-5793(98)00191-4;
 RX Grauso M., Culetto E., Combes D., Fedon Y., Toutant J.P., Arpagaus M.;
 RT "Existence of four acetylcholinesterase genes in the nematodes
 Caenorhabditis elegans and Caenorhabditis briggsae."; FEBS Lett. 424:279-284 (1998).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RA Grauso M., Culetto E., Fedon Y., Combes D., Toutant J.P., Arpagaus M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG Wormbase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating Biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018 (1998).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Moesener J., Graves T., Keppler D.;
 RT "The sequence of C. elegans comid Y44E3A."; Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG Wormbase Consortium;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL: AF025378; AAC14016.2; -;
 DR EMBL: AF106589; AAC78228.2; -;
 DR PIR: T33842; T33842.
 DR PIR: T37255; T37255.
 DR HSSP: P06276; 1P0P.
 DR Wormbase: WBGene0000036; ace-2.
 DR WormPep: Y44E3A.2; CE28363.
 DR GO: GO:0003990; F:acetylcholinesterase activity; IEA.
 DR GO: GO:0004104; F:cholinesterase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser esters.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLNSTRASE.
 DR PROSITE: PS00122; CARBOXYLSESTERASE__B_1; 1.
 KW Hydrolase.
 SQ SEQUENCE 629 AA; 70863 MW; 74940F512FEDF869 CRC64;
 QY 1 MRAPVI 6
 DB 1 MRAPVI 6

Query Match 100.0%; Score 29; DB 2; Length 629;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 06PD31 PRELIMINARY; PRT; 939 AA.
 AC 06PD31;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Caesvant T.L., Schetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whaley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.,
 RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywinski M.I., Skalka U., Smalls D.E., Scherach A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC058971; AAH58971.1; -;
 DR InterPro: IPR006933; HAP1_N.

DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR010978; tRNA_binding_arm.
 DR Pfam; PF04849; HAP1.N.1.
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 939 AA; 104466 MW; 64B1D5D34DF36FCB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 939;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||
 Db 916 MRAPVI 921

RESULT 7
 Q80TL6 PRELIMINARY; PRT; 947 AA.

AC Q80TL6; (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DE KIAA1042 protein (Fragment).
 GN Name=KIAA1042;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
 Nakajima D., Nagase T., Ohara O., Koga H.;
 RT Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT 11. The complete nucleotide sequences of 400 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries."
 RL DNA Res. 10:35-48(2003).

DR EMBL; AK122426; BAC65708.1;
 DR GO; GO:0005634; C:nucleus; ISS.
 DR GO; GO:0005886; C:plasma membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0005102; F:receptor binding; ISS.
 DR GO; GO:0006493; P:O-linked glycosylation; ISS.
 DR GO; GO:0006005; P:protein targeting; ISS.
 DR InterPro; IPR006933; HAP1.N.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR010978; tRNA_binding_arm.
 DR Pfam; PF04849; HAP1.N.1.
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 947 AA; 105486 MW; 0987284C6ACF23A5 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 947;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||
 Db 924 MRAPVI 929

RESULT 8
 RHBI_RAT STANDARD; PRT; 164 AA.

AC Q88779;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 23-OCT-2004 (Rel. 45, Last annotation update)
 DE Rhomboid-related protein 1 (BC 3.4.21.-) (RRP) (rhomboid-like protein

DE 1) (Fragment).
 GN Name=Rhbdl1; Synonyms=Rhbdl;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Intestinal epithelium;
 RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;

RA Pascall J.C., Brown K.D.;
 RT "Characterization of a mammalian cDNA encoding a protein with high
 RT sequence similarity to the Drosophila regulatory protein Rhomboid.";
 RL FEBS Lett. 429:337-340(1998).

CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis
 CC and the subsequent release of functional polypeptides from their
 CC membrane anchors (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.

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DR EMBL; Y17258; CAA76716.1; -.
 DR MEROPS; S54.005; -.
 DR InterPro; IPR002610; Rhomboid_like.
 DR Pfam; PF01694; Rhomboid; 1.
 KW Hydrolase; Protease; Serine protease; Transmembrane.

FT TRANSMEM 1 1
 FT TRANSMEM 32 30 Potential.
 FT TRANSMEM 56 76 Potential.
 FT TRANSMEM 120 140 Potential.
 FT ACT SITE 60 60 Charge relay system (By similarity).
 FT ACT SITE 125 125 Charge relay system (By similarity).
 FT NON_TER 164 164
 SQ SEQUENCE 164 AA; 17662 MW; CF62ACB3BC92910 CRC64;

Query Match 96.6%; Score 28; DB 1; Length 164;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||
 Db 52 MRAPV 57

RESULT 9

Q6FD44 PRELIMINARY; PRT; 231 AA.

AC Q6FD44;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocName=AC1AD1133;
 OS Acinetobacter sp. (strain ADP1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 NCBI_TaxID=62977;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Barbe V., Vallienet D., Fonknechten N., Kreimeyer A., Oztas S.,
 RA Labarre L., Crivellier S., Robert C., Duprat S., Mincker P.,
 RA Ormston L.N., Weisenbach J., Marliere P., Cohen G.N., Medigue C.;
 RT "Unique features revealed by the genome sequence of Acinetobacter sp.
 RT ADP1, a versatile and naturally transformation competent bacterium.";
 RT Nucleic Acids Res. 0:0-0(2004).

DR EMBL, C8543861; CAG68015.1; -.
 DR InterPro; IPR007055; TAD.
 DR Pfam; PF04972; BON; 1.
 DR PROSITE; PSS0914; BON; 1.
 KW Complete proteome.
 SQ SEQUENCE 231 AA; 24680 MW; 7FCDAFCAPDA5E319F CRC64;

Query Match
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6
 |||||:
 136 MRAPV 141

Db

RESULT 10
 RBH1 MOUSE STANDARD; PRT; 373 AA.
 ID RBH1_MOUSE
 AC 08VCB2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RBP) (Rhomboid-like protein 1).
 GN Name=Rbhd1; Synonyms=Rbhd1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Retina;
 MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klanner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein U.E., Jones S.U.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis
 and the subsequent release of functional polypeptides from their
 membrane anchors (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, BC021549; AAH21549.1; -.
 DR MEROPS; S54.005; -.
 DR MGD; MGI:2384891; Rbhd1.
 DR InterPro; IPR002048; EF_Hand.
 DR InterPro; IPR010963; EF_Hand_like.

DR InterPro; IPR002610; Rhomboid_like.
 DR Pfam; PF01694; Rhomboid; 1.
 KW Hydrolase; Protease; Serine protease; Transmembrane.
 DR TRANSMEM 131 151
 FT TRANSMEM 196 216
 FT TRANSMEM 219 239
 FT TRANSMEM 243 263
 FT TRANSMEM 275 294
 FT TRANSMEM 307 327
 FT TRANSMEM 340 360
 FT ACT SITE 199 199
 FT ACT SITE 247 247
 FT ACT SITE 312 312
 SQ SEQUENCE 373 AA; 41766 MW; 1FAE538B3A363D2A CRC64;

Query Match
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6
 |||||:
 239 MRAPV 244

Db

RESULT 11
 ID 08P9FS PRELIMINARY; PRT; 376 AA.
 AC 08P9FS;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Flagellar protein.
 GN Name=flhB; OrderedLocNames=XCC1910;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Camarava F., Cardozo J., Chambergo F., Clapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madelira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Melanda J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Secubal J.C., Kiteajina J.P.P.
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities.";
 RT Nature 417:459-463(2002).
 DR EMBL; A5012294; AAM4119.1; -.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0009306; P-protein secretion; IEA.
 DR InterPro; IPR006135; Bac_Export_2.
 DR InterPro; IPR006136; FlhB.
 DR Pfam; PF01312; Bac_export_2; 1.
 DR PRINTS; PRO0950; TYP31MSPROT.
 KW TIGRPFAMs; TIGR00328; flhB; 1.
 KW Complete proteome.
 SQ SEQUENCE 376 AA; 41490 MW; 406778385A158910 CRC64;

Query Match
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPV1 6
 Db 285 MRAPV 290

RESULT 12
 YTRL EBV STANDARD; PRT; 425 AA.
 ID P30119;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical BTRF1 protein.
 GN Name=BTRF1;
 OS Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84270667; PubMed=6087149;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tufnell P.S., Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1984).
 CC -1- SIMILARITY: Belongs to the herpesviruses BTRF1 family.
 CC -----
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 CC -----
 CC DR EMBL; V01555; CAA24796.1; -.
 CC DR PIR; S33045; S33045.
 CC DR InterPro; IPR006772; Herpes_BTRF1.
 CC DR Pfam; PF04682; Herpes_BTRF1; 1.
 CC KW Hypothetical protein.
 CC SQ SEQUENCE 425 AA; 46711 MW; 0ECBE5FD30495BD CRC64;

Query Match 96.64; Score 28; DB 1; Length 425;
 Best Local Similarity 83.33; Prcd. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPV1 6
 Db 87 MRAPV1 92

RESULT 13
 Q777C1 PRELIMINARY; PRT; 425 AA.
 ID Q777C1;
 AC Q777C1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE BTRF1 protein (Fragment).
 GN Name=BTRF1;
 OS Human herpesvirus 4 (Epstein-Barr virus).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10376;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84270667; PubMed=6087149;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tufnell P.S., Barrell B.G.;

RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=88283646; PubMed=2840285;
 RA Laux G., Periclaudet M., Farrell P.J.,
 RT "A spliced Epstein-Barr virus gene expressed in immortalized
 RT lymphocytes is created by circularization of the linear viral
 RT genome.";
 RL EMBO J. 7:769-774(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=82014887; PubMed=6269068;
 RA Arrand J.R., Rymo L., Walsh J.E., Bjorck E., Lindahl T., Griffin B.E.;
 RT "Molecular cloning of the complete Epstein-Barr virus genome as a set
 RT of overlapping restriction endonuclease fragments.";
 RL Nucleic Acids Res. 9:2999-3014(1981).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=82059504; PubMed=7301588;
 RA Kozak M.;
 RT "Possible role of flanking nucleotides in recognition of the AUG
 RT initiator codon by eukaryotic ribosomes.";
 RL Nucleic Acids Res. 9:5233-5252(1981).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=83109311; PubMed=6296170;
 RA Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;
 RT "Sequence analysis and in vitro transcription of portions of the
 RT Epstein-Barr virus genome.";
 RL J. Cell. Biochem. 19:267-274(1982).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=83169725; PubMed=6300857;
 RA Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
 RT "Homologous upstream sequences near Epstein-Barr virus promoters.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=85035713; PubMed=6092825;
 RA Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
 RT "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
 RT Epstein-Barr virus.";
 RL Mol. Biol. Med. 1:21-45(1983).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=85060424;
 RA Seguin C., Farrell P.J., Barrell B.G.;
 RT "DNA sequence and transcription of the BamHI fragment B region of B95-
 RT 8 Epstein-Barr virus.";
 RL Mol. Biol. Med. 1:369-392(1983).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=83294686; PubMed=6310141;
 RA Jiang K.T., Hayward S.D.;
 RT "Organization of the Epstein-Barr virus DNA molecule. III. Location of
 RT the p3HR-1 deletion junction and characterization of the NotI repeat
 RT units that form part of the template for an abundant 12-O-
 RT tetradecanoylphorbol-13-acetate-induced mRNA transcript.";
 RL J. Virol. 48:135-148(1983).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=85060428; PubMed=6094955;
 RA Bankier A.T., Deininger P.L., Satchwell S.C., Baer R., Farrell P.J.;

RA Barrell B.G.;
 RT "DNA sequence analysis of the EcoRI DheI fragment of B95-8 Epstein-Barr virus containing the terminal repeat sequences.";
 RL Mol. Biol. Med. 1:425-445(1983).
 [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=20311111; PubMed=10872327;
 RA Farrell P.J., Bankier A., Seguin C., Deininger P., Barrell B.G.;
 RT "Latent and lytic cycle promoters of Epstein-Barr virus.";
 RL EMBL J. 2:1331-1338(1983).
 [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84207939; PubMed=6327290;
 RA Jones M.D., Foerster L., Sheedy T., Griffin B.E.;
 RT "The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion similar to that observed in a non-transforming strain (P3HR-1) of the virus.";
 RL EMBL J. 3:813-821(1984).
 [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84236104; PubMed=6203743;
 RA Biggin M., Farrell P.J., Barrell B.G.;
 RT "Transcription and DNA sequence of the BamHI L fragment of B95-8 Epstein-Barr virus.";
 RL EMBL J. 3:1083-1090(1984).
 [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84222045; PubMed=6328526;
 RA Yates J., Warren N., Reisman D., Sugden B.;
 RT "A cis-acting element from the Epstein-Barr viral genome that permits stable replication of recombinant plasmids in latently infected cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).
 [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84247360; PubMed=6330697;
 RA Gibson T., Stockwell P., Ginsburg M., Barrell B.;
 RT "Homology between two EBV early genes and HSV ribonucleotide reductase and 38X genes.";
 RL Nucleic Acids Res. 12:5087-5099(1984).
 [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=87289053; PubMed=3039467;
 RA Bodescot M., Perricaudet M.;
 RT "Clustered alternative splice sites in Epstein-Barr virus RNAs.";
 RL Nucleic Acids Res. 15:5887-5887(1987).
 [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=91021056; PubMed=2171209;
 RA Parker B.D., Bankier A., Satchwell S., Barrell B., Farrell P.J.;
 RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region.";
 RL Virology 179:339-346(1990).
 [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=87289053; PubMed=3039467;
 RA Hattall G.F., Barrell B.G., Quinn J., McGeoch D.;
 RT "Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases." [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RA Birne U.K., Aron W., Farrell P.J.;
 RT "Induction of Epstein-Barr virus late promoters on small plasmids in the EBV late lytic cycle requires ori Lvt.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AJ507799; CAD53449.1; -.

DR InterPro; IPR006772; Herpes_BTRF1.
 DR Pfam; PF04682; Herpes_BTRF1; 1.
 FT NON_TER 1 1
 FT NON_TER 425 425
 SQ SEQUENCE 425 AA; 46711 MW; 0ECBSE5FD30495BD CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 425;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 87 MRAPVI 92
 RESULT 14
 ID RBH1_HUMAN STANDARD; PRT; 438 AA.
 AC 075783; Q9NQ85;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein 1).
 GN Name=RHBDL1; Synonyms=RHBDL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Leukemia;
 RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;
 RA Pascali J.C., Brown K.D.;
 RT "Characterization of a mammalian cDNA encoding a protein with high sequence similarity to the Drosophila regulatory protein Rhomboid.";
 RL FEBS Lett. 429:337-340(1998).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21096910; PubMed=1115797; DOI=10.1093/hmg/10.4.339;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tifarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2 kb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis and the subsequent release of functional polypeptides from their membrane anchors (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O75783-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O75783-2; Sequence=VSP_005372;
 CC -1- TISSUE SPECIFICITY: Detected in heart, brain, skeletal muscle and kidney.
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.
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 CC -----
 DR EMBL; Y17108; CAI76629.1; -.
 DR EMBL; AJ772344; CAC00640.1; -.
 DR EMBL; AE006464; AAK61241.1; -.
 DR MEROPS; S54_005; -.
 DR Genew; HGNC:10007; RHBDL1.

DR MIM; 603264; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR002048; EF-hand-like.
 DR InterPro; IPR010983; EF-hand-like.
 DR Pfam; PF01694; Rhomboid; 1.
 DR Alternative splicing; Hydrolyase; Protease; Serine protease;
 KM Transmembrane
 FT TRANSMEM 196 216 Potential.
 FT TRANSMEM 262 282 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 308 328 Potential.
 FT TRANSMEM 340 359 Potential.
 FT TRANSMEM 372 392 Potential.
 FT TRANSMEM 405 425 Potential.
 FT ACT_SITE 264 264 Charge relay system (By similarity).
 FT ACT_SITE 312 312 Charge relay system (By similarity).
 FT ACT_SITE 377 377 Charge relay system (By similarity).
 FT VARSPLIC 1 77 MGRVEDGGTTELEDMDPGTSALPAPQIKGPREOTGTGPTL
 FT DRSSLIQIIOE (in isoform 2).
 FT /FTid=VSP_005372.
 SQ SEQUENCE 438 AA; 48314 MW; A7644AD3644A2F6 CRC64;
 Query Match 96.6%; Score 28; DB 1; Length 438;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPI 6
 Db 304 MRAPIV 309

RESULT 15
 Q8NT69 PRELIMINARY; PRT; 541 AA.
 AC Q8NT69; Q6WT59;
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 28, last annotation update)
 DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE ResB protein required for cytochrome c biosynthesis (Membrane protein
 required for cytochrome c biosynthesis).
 GN OorediocuNames=Cg10441, CG0523;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OC NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX PubMed=1294826; DOI=10.1016/S0168-1656(03)00154-8;
 RA Kallinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
 Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
 Goessmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
 McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
 Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
 Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
 and its impact on the production of L-aspartate-derived amino acids
 and vitamins."
 RL J. Biotechnol. 104:5-25 (2003).
 DR EMBL; AP005275; BAB97834.1; -.
 DR EMBL; BX927149; CAF19157.1; -.
 DR InterPro; IPR007816; ResB.
 DR Pfam; PF05140; ResB; 1.

KM Complete proteome.
 SQ SEQUENCE 541 AA; 61244 MW; 37F42BA0A74F78BB CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 541;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPI 6
 Db 103 MRAPIV 108

Search completed: April 25, 2005, 20:33:58
 Job time : 5.09978 secs

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OM protein - protein search, using SW model

Run on: April 25, 2005, 20:24:31 ; Search time 17.1053 Seconds

(without alignments)
484.413 Million cell updates/sec

Title: US-10-029-926D-7

Perfect score: 576
Sequence: 1 SELTOPPAVSVALGQTVRIT.....SGNHVFGGKTLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/aa/PTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	576	100.0	278	3	US-09-260-527-3
2	576	100.0	280	3	US-09-260-527-1
3	576	100.0	309	3	US-09-079-029-9
4	576	100.0	312	3	US-09-079-029-10
5	558	96.9	108	4	US-09-720-493-4
6	554	96.2	111	4	US-09-203-768A-8
7	537	93.2	109	2	US-08-652-816A-16
8	531.5	92.3	109	2	US-08-665-202-34
9	531.5	92.3	109	4	US-09-315-574-34
10	525	91.1	101	4	US-09-726-219A-168
11	502	87.2	97	2	US-08-665-202-35
12	502	87.2	97	4	US-09-315-574-35
13	494.5	85.9	104	3	US-08-793-450-6
14	494.5	85.9	104	3	US-09-240-374-49
15	487	84.5	106	3	US-09-240-374-48
16	480	83.3	106	3	US-09-240-374-47
17	475.5	82.6	102	4	US-09-726-219A-174
18	473	82.1	106	3	US-09-240-374-47
19	473	82.1	106	3	US-09-240-374-50
20	471	81.8	103	2	US-08-273-146-71
21	448.5	77.9	108	3	US-09-025-769B-20
22	448.5	77.9	108	4	US-09-490-070A-20
23	448.5	77.9	108	4	US-09-490-153-20
24	448.5	77.9	108	4	US-09-490-324-20
25	443.5	77.0	105	1	US-08-488-113B-157
26	443.5	77.0	105	1	US-08-477-484B-157
27	443.5	77.0	105	1	US-08-107-669D-21

28	443.5	77.0	105	1	US-08-472-788A-21	Sequence 21, Appl
29	443.5	77.0	105	2	US-08-477-531B-21	Sequence 21, Appl
30	443.5	77.0	105	2	US-08-646-360-157	Sequence 157, Appl
31	443.5	77.0	105	2	US-08-082-842A-21	Sequence 21, Appl
32	443.5	77.0	105	3	US-08-839-765-157	Sequence 157, Appl
33	443.5	77.0	105	3	US-09-136-389-157	Sequence 157, Appl
34	443.5	77.0	105	3	US-09-610-838-157	Sequence 157, Appl
35	443.5	77.0	105	4	US-09-711-485-157	Sequence 157, Appl
36	441	76.6	125	4	US-09-471-276-1249	Sequence 1249, Ap
37	423	73.4	108	1	US-08-360-125-12	Sequence 12, Appl
38	423	73.4	108	2	US-08-450-578-12	Sequence 12, Appl
39	423	73.4	108	2	US-09-017-628-12	Sequence 12, Appl
40	423	73.4	108	2	US-09-014-880-12	Sequence 12, Appl
41	423	73.4	108	4	US-08-450-363-12	Sequence 12, Appl
42	423	73.4	108	4	US-09-467-903-12	Sequence 12, Appl
43	420	72.9	118	4	US-09-513-999C-4175	Sequence 4175, Ap
44	419	72.7	109	3	US-09-157-370-5	Sequence 5, Appl
45	397	68.9	107	3	US-09-025-769B-34	Sequence 34, Appl

ALIGNMENTS

```
RESULT 1
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0.
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match          100.0%; Score 576; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SELTOPPAVSVALGQTVRITCGDSLSRSYVAYQKPGAPVLYIGKNNRSGIPDRF 60
      |||||
DB      154 SELTOPPAVSVALGQTVRITCGDSLSRSYVAYQKPGAPVLYIGKNNRSGIPDRF 213
      |||||
QY      61 SGSSSGNTASLTITGAQAEDEADYYCNSRRSSGNHVVFGGKTLTVLGAAA 111
      |||||
DB      214 SGSSSGNTASLTITGAQAEDEADYYCNSRRSSGNHVVFGGKTLTVLGAAA 264
      |||||

RESULT 2
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 280
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
OTHER INFORMATION: phase display library known as the Synthetic scFv
OTHER INFORMATION: library (#1) from the Centre for Protein
OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match 100.0%; Score 576; DB 3; Length 280;
Best local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60
DB 156 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 215
QY 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 111
DB 216 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 266

RESULT 3

US-09-079-029-9
Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-9

Query Match 100.0%; Score 576; DB 3; Length 309;
Best local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60
DB 156 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 215
QY 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 111
DB 216 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 266

DB 176 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 235
QY 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 111
DB 236 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 286

RESULT 4

US-09-079-029-10
Sequence 10, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-10

Query Match 100.0%; Score 576; DB 3; Length 312;
Best local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60
DB 179 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 238
QY 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 111
DB 239 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFGGTRKLTVLGAAA 289

RESULT 5

US-09-720-493-4
Sequence 4, Application US/09720493
Patent No. 6827925
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J.
APPLICANT: Tempest, Philip R.
APPLICANT: Hollet, Thor L.
APPLICANT: Main, Sarah H.
APPLICANT: Jackson, Helen
APPLICANT: Darmon, Olekan

TITLE OF INVENTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CP577533
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-720-493-4

Query Match 96.9%; Score 558; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYKNNRPSGIPDRF 60
|||
DB 2 SEITDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYKNNRPSGIPDRF 61
|||
QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTLTVL 107
|||
DB 62 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTLTVL 108
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RESULT 6
US-09-203-768A-8
Sequence 8, Application US/09203768A
Patent No. 6787638
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Mackins, Jeffrey D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
FILE REFERENCE: P-IX 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 8
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
US-09-203-768A-8

Query Match 96.2%; Score 554; DB 4; Length 111;
Best Local Similarity 99.1%; Pred. No. 5.8e-46;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYKNNRPSGIPDRF 60
|||
DB 2 SEITDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYKNNRPSGIPDRF 61
|||
QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTLTVL 108
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DB 62 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTLTVL 109
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RESULT 7
US-08-652-816A-16
Sequence 16, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McGafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-16

Query Match 93.2%; Score 537; DB 2; Length 109;
Best Local Similarity 96.2%; Pred. No. 2.4e-44;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYKNNRPSGIPDRF 60
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DB 2 SEITDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYKNNRPSGIPDRF 61
|||
QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTLTVL 106
|||
DB 62 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTLTVL 107
|||

RESULT 8
US-08-655-202-34
Sequence 34, Application US/08655202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-34
Query Match 92.3%; Score 531.5; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 8.1e-44;
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 1 SEITDPAVSVALGQTVRTICQSDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60
DB 1 SEITDPAVSVALGQTVRTICQSDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGN-HVPGGKTKLTVLG 108
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHPVWFGGKTKVTVLG 109
RESULT 9
US-09-315-574-34
Sequence 34, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-34
Query Match 92.3%; Score 531.5; DB 4; Length 109;
Best Local Similarity 95.4%; Pred. No. 8.1e-44;
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 1 SEITDPAVSVALGQTVRTICQSDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60
DB 1 SEITDPAVSVALGQTVRTICQSDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGN-HVPGGKTKLTVLG 108
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHPVWFGGKTKVTVLG 109
RESULT 10
US-09-726-219A-168
Sequence 168, Application US/09726219A
Patent No. 6806079
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kaspar
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonetti, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12

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; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-168

Query Match      91.1%; Score 525; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEITDPNPAVSVALGQTVRTTCGDSLRSYASWYQKPGAPLVLYGKNNRPSGIPDRF 60
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DB      2 SEITDPNPAVSVALGQTVRTTCGDSLRSYASWYQKPGAPLVLYGKNNRPSGIPDRF 61

QY      61 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHVFGG 100
        |||
DB      62 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHVFGG 101

RESULT 11
US-08-665-202-35
; Sequence 35, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-35

Query Match      87.2%; Score 502; DB 2; Length 97;
Best Local Similarity 99.0%; Pred. No. 4.8e-41;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SEITDPNPAVSVALGQTVRTTCGDSLRSYASWYQKPGAPLVLYGKNNRPSGIPDRF 60
        |||
DB      1 SEITDPNPAVSVALGQTVRTTCGDSLRSYASWYQKPGAPLVLYGKNNRPSGIPDRF 60

QY      61 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHV 97
        |||
DB      61 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHV 97

RESULT 12
US-09-315-574-35
; Sequence 35, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-35

Query Match      87.2%; Score 502; DB 4; Length 97;
Best Local Similarity 99.0%; Pred. No. 4.8e-41;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 SELTODPAVSVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60
Db 1 SSILOPAPASVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60
QY 61 SGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVV 97
Db 61 SGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVV 97

RESULT 13

US-08-793-450-2
; Sequence 2, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABIBI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-2

Query Match 85.9%; Score 494.5; DB 3; Length 104;
Best Local Similarity 90.7%; Pred. No. 2,7e-40;
Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 2 ELTODPAVSVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 61
Db 3 ELTODPAVSVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 62
QY 62 SGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVVFGGSKTLTVLG 108
Db 63 SGSSSGNTASLITGAQAEDEADYYCNSGK-----VGGGSKTLTVLG 104

RESULT 14
US-08-793-450-6
; Sequence 6, Application US/08793450

; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABIBI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-6

Query Match 85.9%; Score 494.5; DB 3; Length 238;
Best Local Similarity 90.7%; Pred. No. 6,9e-40;
Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 2 ELTODPAVSVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 61
Db 22 ELTODPAVSVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 81
QY 62 SGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVVFGGSKTLTVLG 108
Db 82 SGSSSGNTASLITGAQAEDEADYYCNSGK-----VGGGSKTLTVLG 123

RESULT 15
US-09-240-274-49
; Sequence 49, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain J04
US-09-240-274-49

```

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Query Match      84.5%; Score 487; DB 3; Length 104;
Best Local Similarity 92.2%; Pred. No. 1,4e-39;
Matches 95; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

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QY 5 ODPVSVVALGQTVRITCGDSDLSRSYYASWTQOKPGQAPLVIVYKNNRPSGIPDRFSGSS 64
DB 4 QDPVSVVALGQTVRITCGDSDLSRSYYASWTQOKPGQAPLVIVYKNNRPSGIPDRFSGSS 63
QY 65 SGN TASLITITGAQAEDEADYYCNSRDSSGNHVVFGGGLTTL 107
DB 64 SGN TASLITITGAQAEDEADYYCSSRGSP--HVAFGGGLTTL 104

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Search completed: April 25, 2005, 21:12:10
Job time : 18.1053 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 68.0521 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926d-7

Sequence: 1 SEITQDPAVSVALGQTVRIT.....SGNHVFGGKTLVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	5 ABG78132	ABG78132 Human Fv
2	576	100.0	111	5 ABG91823	ABG91823 Human ant
3	576	100.0	112	8 ADJ57867	ADJ57867 Common li
4	576	100.0	209	5 AAU98017	AAU98017 Human ace
5	576	100.0	249	8 ADR23324	ADR23324 Human CD7
6	576	100.0	260	5 ABG92023	ABG92023 Antibody
7	576	100.0	263	5 ABG92024	ABG92024 Antibody
8	576	100.0	266	5 ABG92020	ABG92020 Human ant
9	576	100.0	277	5 ABG78150	ABG78150 Human Fv
10	576	100.0	277	5 ABG78328	ABG78328 Human Fv
11	576	100.0	277	5 ABG92019	ABG92019 Human ant
12	576	100.0	277	5 ABG91841	ABG91841 Human ant
13	576	100.0	277	8 ADI28366	ADI28366 Human scf
14	576	100.0	278	8 ADI28367	ADI28367 Human scf
15	576	100.0	280	4 AAEO2186	AAEO2186 PAM2 sing
16	576	100.0	280	8 ADI28368	ADI28368 Human scf
17	576	100.0	280	8 ADJ57363	ADJ57363 P-selecti
18	576	100.0	282	4 AAEO2185	AAEO2185 PAM1 sing
19	576	100.0	309	2 AAAB3322	AAAB3322 Single ch
20	576	100.0	309	5 ABB09603	ABB09603 Amino aci
21	576	100.0	309	6 ABG74384	ABG74384 Single ch
22	576	100.0	309	7 ADG96737	ADG96737 Human sin
23	576	100.0	309	8 ADO40446	ADO40446 Human sin
24	576	100.0	312	2 AAAB3323	AAAB3323 Single ch
25	576	100.0	312	5 ABB09604	ABB09604 Amino aci

26	576	100.0	312	6 ABG74385	ABG74385 Single ch
27	576	100.0	312	7 ADG98738	ADG98738 Human sin
28	576	100.0	312	8 ADO40447	ADO40447 Human sin
29	570	99.0	274	8 ADO25153	ADO25153 Melanoma
30	568	98.6	110	8 ADS12488	ADS12488 Human IGF
31	568	98.6	110	8 ADS12484	ADS12484 Human IGF
32	568	98.6	215	8 ADR23362	ADR23362 Human CD7
33	565	98.1	229	2 AAAB9694	AAAB9694 Human scf
34	565	98.1	254	2 AAAB9693	AAAB9693 Human scf
35	564	97.9	108	4 AAG62939	AAG62939 Amino aci
36	564	97.9	108	5 AAG80198	AAG80198 Human gp9
37	564	97.9	109	4 AAU02513	AAU02513 Ant1-adip
38	564	97.9	236	2 AAAB9690	AAAB9690 Human scf
39	564	97.9	237	2 AAAB9691	AAAB9691 Human scf
40	564	97.9	237	5 ABPA6101	ABPA6101 Human Bly
41	564	97.9	237	5 ABPA5930	ABPA5930 Human Bly
42	564	97.9	237	7 ADG96928	ADG96928 Single ch
43	564	97.9	237	7 ADG96757	ADG96757 Single ch
44	564	97.9	238	5 ABPA5896	ABPA5896 Human Bly
45	564	97.9	238	7 ADG96723	ADG96723 Single ch

ALIGNMENTS

RESULT 1	ABG78132	ABG78132 standard; protein; 111 AA.
ID	ABG78132	ABG78132 standard; protein; 111 AA.
AC	ABG78132	
DT	15-NOV-2002	(first entry)
XX		
DE	Human Fv molecule hypervariable region related peptide #7.	
XX		
KW	Human Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200259264-A2.	
XX		
PD	01-AUG-2002.	
XX		
PF	31-DEC-2001; 2001WO-US049440.	
XX		
PR	29-DEC-2000; 2000US-00751181.	
XX		
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
XX		
PI	Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Lavanon A; Plakshin D, Peretz T;	
XX		
DR	WPI; 2002-619166/66.	
PT	Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other cells.	
PT		
XX		
PS	Disclosure; Page 150; 232pp; English.	
XX		
CC	The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scfv) or a disulfide Fv (dsfv). The peptide, optionally in association with or attached, coupled, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,	

CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

XX
 CC
 SQ Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.8e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCCGDSLRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60
 DB 1 SEITDPAVSVALGQTVRITCCGDSLRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60

QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111

RESULT 2

ABG91823
 ID ABG91823 standard; protein; 111 AA.

XX
 AC ABG91823;

DT 04-DEC-2002 (first entry)

XX
 DE Human antibody fragment #7.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX MO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Stanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

XX Disclosure; Page 227-228; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility

CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

XX
 CC
 SQ Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.8e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCCGDSLRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60
 DB 1 SEITDPAVSVALGQTVRITCCGDSLRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60

QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111

RESULT 3

ADJ57867
 ID ADJ57867 standard; protein; 112 AA.

XX
 AC ADJ57867;

DT 06-MAY-2004 (first entry)

XX Common light variable chain protein of B29, II-2 and I-2.

XX Cytostatic; immunosuppressive; Antibacterial; Virucide; Fungicide;
 KW Antiparasitic; auto-immune disease; cancer; neoplastic disorder;
 KW leukemia.

XX Synthetic.

XX WO2004009618-A2.

XX 29-JAN-2004.

XX 15-JUL-2003; 2003WO-EP007690.

XX 18-JUL-2002; 2002EP-00077953.

XX 18-JUL-2002; 2002US-0397066P.

XX 27-MAY-2003; 2003WO-EP050201.

XX (CRUC-) CRUCELL HOLLAND BV.

XX Van Berkel PHC, Brus RHP, Bout A, Logtenberg T;

XX WPI; 2004-132914/13.

XX N-PSDB; ADJ57866.

PT Producing mixture of antibodies in recombinant host comprises expressing
 PT nucleic acid sequence(s) encoding light chain and three different heavy
 PT chains capable of pairing with light chain in recombinant host cell.

XX Disclosure; SEQ ID NO 18; 186pp; English.

XX The present invention relates to producing a mixture of antibodies in a
 CC recombinant host comprises expressing in a recombinant host cell a
 CC nucleic acid sequence or nucleic acid sequences encoding a light chain
 CC and at least three different heavy chains that are capable of pairing
 CC with a light chain. The method is useful for producing a mixture of
 CC antibodies in a recombinant host, is useful for the preparation of a
 CC medicament for use in the treatment or diagnosis of a disease or disorder
 CC in a human or animal. The antibodies are useful for treating auto-immune

CC disease and cancer such as solid tumors of the brain, head and neck,
 CC breast, prostate, colon, lung, etc.; hematologic tumors such as B-cell
 CC tumors, neoplastic disorders such as leukemia, lymphoma, sarcoma,
 CC carcinoma, neural cell tumors, myelomas, melanomas, neuroblastomas, etc.,
 CC and are also useful for treating graft-versus-host rejections, infectious
 CC diseases due to pathogenic bacteria such as multidrug resistant
 CC staphylococcus aureus, fungi such as Candida albicans, as prophylaxis
 CC against viruses such as rabies virus, for treating or preventing disease
 CC caused by adenoviruses, respiratory syncytium virus, and for treating
 CC diseases caused by unicellular or multicellular parasites. The method
 CC enables exploring many combinations simultaneously, where the
 CC combinations include the presence of bispecific antibodies in the
 CC produced mixture. The present sequence represents the common light
 CC variable chain of B28, II-2 and I-2.

XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 576; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.8e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60
 DB 2 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDRF 61

QY 61 SGSSSGNTASTLTITGAQAEDEADYYCNSRPSGNNHVFPGGKTLTVLGAA 111
 DB 62 SGSSSGNTASTLTITGAQAEDEADYYCNSRPSGNNHVFPGGKTLTVLGAA 112

RESULT 4
 AAU98017
 AAU98017 standard; protein; 209 AA.

AC AAU98017;
 DT 27-AUG-2002 (first entry)
 XX
 XX Human acetylcholinesterase antibody PD-antihASP 1.

DE Human acetylcholinesterase antibody PD-antihASP 1;
 KW Human; synaptic acetylcholinesterase; PD-antihASP 1; antibody;
 KW single-chain variable region; scFv; AChE-S;
 KW heavy chain variable region; progressive neuromuscular disorder;
 KW muscle distortion; muscle re-innervation; myasthenia gravis;
 KW neuromuscular junction abnormality; Eaton-Lambert disease;
 KW muscular dystrophy; amyotrophic lateral sclerosis; ALS;
 KW post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
 KW post-stroke sclerosis; post-injury muscle damage;
 KW excessive re-innervation.

XX
 OS Homo sapiens.
 XX
 PN WO200246422-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 22-MAY-2001; 2001WO-IL000464.
 XX
 PR 04-DEC-2000; 2000IL-00140071.
 XX
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX
 PI Soreq H, Plores CF, Nissim A;
 XX
 DR WPI; 2002-463832/49.
 DR N-PSDB; ABK52915.
 XX
 PT Nucleic acid sequence coding for a single-chain variable fragment (scFv)
 PT antibody that has specific affinity for the synaptic variant of
 PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular
 PT disorder, e.g. Myasthenia gravis.
 XX
 PS Claim 11; Page 61-63; 73pp; English.

XX
 CC The invention relates to a nucleic acid sequence coding for a single-
 CC chain variable fragment (scFv) antibody that has specific affinity for
 CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv
 CC antibody consists essentially of a polypeptide comprising the binding
 CC portion of the heavy chain variable region of an antibody. Also included
 CC are an expression vehicle comprising a nucleic acid sequence coding for a
 CC scFv antibody that has specific affinity for the synaptic variant of AChE
 CC -S, an scFv antibody specifically recognising and binding to the synaptic
 CC variant of AChE-S and a method for the diagnosis of a progressive
 CC neuromuscular disorder in a mammal, comprising obtaining a sample from
 CC the mammal and detecting intensified expression of at least one of the
 CC AChE variants in the sample. The single-chain Fv antibody is useful for
 CC diagnosing a progressive neuromuscular disorder which involves any one of
 CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
 CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
 CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
 CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post
 CC -stroke sclerosis, post-injury muscle damage, excessive re-innervation,
 CC or post-exposure to AChE inhibitors. The present sequence represents an
 CC anti-AChE scFv antibody, PD-antihASP 1

XX
 SQ Sequence 209 AA;

Query Match 100.0%; Score 576; DB 5; Length 209;
 Best Local Similarity 100.0%; Pred. No. 5.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60
 DB 76 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPLVITYGKNNRPSGIPDRF 135

QY 61 SGSSSGNTASTLTITGAQAEDEADYYCNSRPSGNNHVFPGGKTLTVLGAA 111
 DB 136 SGSSSGNTASTLTITGAQAEDEADYYCNSRPSGNNHVFPGGKTLTVLGAA 186

RESULT 5
 ADR23324
 ADR23324 standard; protein; 249 AA.

AC ADR23324;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 XX Human CD72-targeted scFv Sc02-025.
 DE Human CD72-targeted scFv Sc02-025.
 XX
 KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytotoxic;
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.

XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 101..112
 FT /label= CDR3
 XX
 PN WO2004067569-A1.
 XX
 PD 12-AUG-2004.
 XX
 PF 27-JAN-2003; 2003WO-EP050004.
 XX
 PR 27-JAN-2003; 2003WO-EP050004.
 XX
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Bakker ABH, Marijssen WE;
 XX
 DR WPI; 2004-580978/56.
 DR N-PSDB; ADR23323.
 XX
 PT New internalizing human binding molecules capable of specifically binding
 PT to CD72, useful for diagnosing and/or treating B-cell associated

PT diseases, such as cancer or autoimmune disorders.

XX Example 3; SEQ ID NO 16; 174pp; English.

XX The present sequence is the protein sequence of Sc02-025, an scFv that
CC specifically recognises human B cell associated antigen CD72. It
CC comprises V_H1 DP07 and V_H11 germline sequences. The scFv was selected
CC from an antibody phage display library using human tonsillar mononuclear
CC cells as target. It was shown to selectively bind to peripheral blood
CC CD19⁺ B cells and to CD72-transfected U937 cells. Plasmid DNA was
CC obtained from the scFv clone and used to determine the scFv nucleic acid
CC and amino acid sequences. Sc02-025 scFv was used to generate CD72-
CC directed human IgG1 antibodies comprising heavy chain ADR23350 and light
CC chain ADR23362 sequences. Such anti-CD72 immunoglobulins or their antigen
CC-binding fragments can be used as internalising human binding molecules
CC of the invention. These internalising human binding molecules are capable
CC of (specifically) binding to CD72 or its antigenic determinant, and
CC preferably bind to CD72 associated with cells. Upon binding to CD72
CC present on the surface of target cells, the binding molecules
CC internalise. In addition to the internalising human binding molecules,
CC the invention provides immunocombinates comprising an internalising human
CC binding molecule and a tag (toxic substance, radioactive substance,
CC liposome and/or enzyme), nucleic acids encoding these, and compositions
CC comprising them. The internalising human binding molecule,
CC immunocombinate, nucleic acid molecule or composition can be used in the
CC diagnosis and/or treatment of a B cell associated disorder or disease,
CC especially a B cell associated cancer and B cell associated autoimmune
CC disorder (claimed).

XX Sequence 249 AA;

XX Query Match 100.0%; Score 576; DB 8; Length 249;
XX Best Local Similarity 100.0%; Pred. No. 6.2e-35;
XX Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRPSGIPDRF 60
DB 139 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRPSGIPDRF 198
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAA 111
DB 199 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAA 249

RESULT 6

ID ABG92023 standard; protein; 260 AA.

XX ABG92023;

DT 04-DEC-2002 (first entry)

XX Antibody protein #3.

XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX metastasis; hypervariable region; autoimmune disease; thrombosis;

XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;

XX myocardial infarction; retinopathic disease; abnormal platelet function;

XX sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
PI Sznathon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.

PS Disclosure; Fig 49; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents an antibody protein of the
CC invention

XX Sequence 260 AA;

XX Query Match 100.0%; Score 576; DB 5; Length 260;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-35;
XX Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRPSGIPDRF 60
DB 136 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRPSGIPDRF 195
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAA 111
DB 196 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAA 246

RESULT 7

ID ABG92024 standard; protein; 263 AA.

XX ABG92024;

DT 04-DEC-2002 (first entry)

XX Antibody protein #4.

XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX metastasis; hypervariable region; autoimmune disease; thrombosis;

XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;

XX myocardial infarction; retinopathic disease; abnormal platelet function;

XX sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 XX
 PA (BIOI-) BIO-TECHNOLOGY GEN CORP.
 PI Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 XX WPI; 2002-674776/72.
 DR
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Fig 50; Opp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 CC
 XX
 SQ Sequence 263 AA;
 Query Match 100.0%; Score 576; DB 5; Length 263;
 Best Local Similarity 100.0%; Pred. No. 6.5e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEITDPAVSVALGQTVRITTCGDSLSRSYASWYQKPGAPVLVIYKKNRPSGIPDRF 60
 DB 133 SEITDPAVSVALGQTVRITTCGDSLSRSYASWYQKPGAPVLVIYKKNRPSGIPDRF 192
 QY 61 SGSSSGNTASLTITGAOAEDEADYYCNSRDSGNHVPFGGKTLTVLGAAA 111
 DB 193 SGSSSGNTASLTITGAOAEDEADYYCNSRDSGNHVPFGGKTLTVLGAAA 243

RESULT 8
 ABG92020
 ID ABG92020 standard; protein; 266 AA.
 AC
 XX ABG92020;
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #204.
 XX
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 OS Homo sapiens.
 XX
 XX
 PN WO200253700-A2.

XX
 XX 11-JUL-2002.
 PD
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 XX
 PA (BIOI-) BIO-TECHNOLOGY GEN CORP.
 PI Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 XX WPI; 2002-674776/72.
 DR
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Page 309-310; Opp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 CC
 XX
 SQ Sequence 266 AA;
 Query Match 100.0%; Score 576; DB 5; Length 266;
 Best Local Similarity 100.0%; Pred. No. 6.6e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEITDPAVSVALGQTVRITTCGDSLSRSYASWYQKPGAPVLVIYKKNRPSGIPDRF 60
 DB 153 SEITDPAVSVALGQTVRITTCGDSLSRSYASWYQKPGAPVLVIYKKNRPSGIPDRF 212
 QY 61 SGSSSGNTASLTITGAOAEDEADYYCNSRDSGNHVPFGGKTLTVLGAAA 111
 DB 213 SGSSSGNTASLTITGAOAEDEADYYCNSRDSGNHVPFGGKTLTVLGAAA 263

RESULT 9
 ABG78150
 ID ABG78150 standard; protein; 277 AA.
 AC
 XX ABG78150;
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #25.
 XX
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX

OS Homo sapiens.
 XX
 XX WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 XX 31-DEC-2001; 2001WO-US049440.
 XX
 XX 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOI-) BIO-TECHNOLOGY GEN CORP.
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plakein D, Peretz T;
 XX WPI; 2002-619166/66.
 XX
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 PS Claim 4; Page 155-156; 232pp; English.
 XX
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments of a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 CC
 XX
 XX Sequence 277 AA;
 SQ
 Query Match 100.0%; Score 576; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 6.9e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYGNRRPSGIPDRF 60
 Db 153 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYGNRRPSGIPDRF 212
 QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGTXTLVGAAA 111
 Db 213 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGTXTLVGAAA 263

RESULT 10

ABG78328
 ID ABG78328 standard; protein; 277 AA.
 XX
 AC ABG78328;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #203.
 XX
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200259264-A2.
 XX

PD 01-AUG-2002.
 XX
 XX 31-DEC-2001; 2001WO-US049440.
 XX
 XX 29-DEC-2000; 2000US-00751181.
 XX
 XX (BIOI-) BIO-TECHNOLOGY GEN CORP.
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plakein D, Peretz T;
 XX WPI; 2002-619166/66.
 XX
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 PS Claim 14; Fig 14; 232pp; English.
 XX
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments of a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 CC
 XX
 XX Sequence 277 AA;
 SQ
 Query Match 100.0%; Score 576; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 6.9e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYGNRRPSGIPDRF 60
 Db 153 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYGNRRPSGIPDRF 212
 QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGTXTLVGAAA 111
 Db 213 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGTXTLVGAAA 263

RESULT 11

ABG92019
 ID ABG92019 standard; protein; 277 AA.
 XX
 AC ABG92019;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #203.
 XX
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 XX WO200253700-A2.
 XX
 XX 11-JUL-2002.
 XX

XX	31-DEC-2001; 2001WO-US049442.
PP	
XX	29-DEC-2000; 2000US-00751181.
XX	
FR	29-DEC-2000; 2000US-0258948P.
XX	
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.
XX	
PI	Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
PI	Szantonon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX	
DR	WPI, 2002-674776/72.
XX	
PT	Novel isolated epitope present on cancer cells and important in
FT	physiological phenomena such as cell rolling, metastasis and
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular
XX	diseases, and cancer.
PS	
XX	Claim 23; Page 308-309; Opp; English.
CC	The invention relates to an isolated epitope present on cancer cells and
CC	important in physiological phenomena such as cell rolling, metastasis and
CC	inflammation, where the epitope is capable of being bound by an antibody,
CC	its antigen-binding fragment or its complex comprising at least one
CC	antibody or its binding fragment having a first hypervariable region. The
CC	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC	diseases, thrombosis, reathenosis, metastasis, growth and/or replication of
CC	tumour or leukaemia cells, increase in number of tumour or leukaemia
CC	cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC	platelet and/or cell-platelet adhesion or aggregation, for increasing
CC	mortality of tumour or leukaemia cells, for increasing the susceptibility
CC	of diseased cells to damage by anti-disease, anti-cancer or anti-
CC	leukaemia agents, or for decreasing the number of tumour or leukaemia
CC	cells in a patient, or in the manufacture of a medicament for the above
CC	mentioned purposes. The epitopes are useful for diagnosing and treating
CC	diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC	diseases, cardiovascular diseases such as myocardial infarction,
CC	retinopathic diseases and other diseases mediated by abnormal platelet
CC	function and diseases caused by sulphated tyrosine-dependent protein-
CC	protein interactions. This sequence represents a human antibody fragment
XX	of the invention
SO	
XX	Sequence 277. AA;
Query Match	100.0%; Score 576; DB 5; Length 277;
Best Local Similarity	100.0%; Pred. No. 6.9e-35;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 SELTDPAYVALGQTVRITCGDSLRSVYSWYQKFGAPVLVIYKNNRPSGIDPRF 60
Db	153 SELTODPAYVALGQTVRITCGDLSRSVYSWYQKFGAPVLVIYKNNRPSGIDPRF 212
OY	61 SGSSSGNNAALTTTCGAODEADADYYCNSRDSSGNHVVGGGTKLTVLGAAA 111
Db	213 SGSSSGNNAALTTTCGAODEADADYYCNSRDSSGNHVVGGGTKLTVLGAAA 263
RESULT 12	
ID	ABG91841
AC	ABG91841;
XX	
DT	04-DEC-2002 (first entry)
XX	
DE	Human antibody fragment #25.
XX	
KM	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM	metastasis; hypervariable region; autoimmune disease; thrombosis;
KM	reathenosis; leukaemia; inflammatory disease; cardiovascular disease;
KM	myocardial infarction; retinopathic disease; abnormal platelet function;
XX	sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.
XX WO200253700-A2.
XX
XX 11-JUL-2002.
XX
XX
XX 31-DEC-2001; 2001WO-US049442.
XX
XX 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
PI Sznitnon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
DR MPI; 2002-674776/72.
XX
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.

Claim 23; Page 233-234; Opp; English.

The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. These epitopes are useful for inhibiting cell rolling. Inflammation, autoimmune diseases, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, reinfarctic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention

Sequence 277 AA:

Query Match 100.0%; Score 576; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-35;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 SELTQDPVSVVALGQTVAITTCGGDSLRSYVASWYOQKPGQAPVLVIYGKNRPSGIPDRF 60
DB 153 SELTQDPAVSVALGCTVAITTCGGDSLRSYVASWYOQKPGQAPVLVIYGKNRPSGIPDRF 212
OY 61 SGSSSGMTASTLTIGAQAEDADYYCNSRDSSGNVTNVCGGPKLTVLGAA 111
DB 213 SGSSSGMTASTLTIGAQAEDADYYCNSRDSSGNHVVFGGPKLTVLGAA 263

RESULT 13
ADI28366
XX ADI28366; standard; protein; 277 AA.
XX
XX ADI28366;
DT 06-MAY-2004 (first entry)
XX
DE Human scFv fragment Y1, binds to platelets.
TW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

```
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX PA (SAVI-) SAVIENT PHARM INC.
XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX DR WPI; 2004-099189/10.
XX PT Composition comprising an agent and/or antibody or its fragment, useful
XX PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
XX PT for inhibiting growth and/or replication of tumor cells or leukemia
XX PT cells.
XX PS Claim 13; SEQ ID NO 1; 58pp; English.
XX CC The present sequence is the protein sequence of human scfv fragment Y1.
XX CC This antibody was identified by screening a human antibody phage library
XX CC that has diversity only in the heavy chain CDR3 regions. Fixed human
XX CC platelets were screened in order to identify antibodies that bind
XX CC platelets. The epitope for Y1 antibody is located between amino acids 272
XX CC and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the
XX CC N-terminal of PSL-1, a receptor for E-, L- and P-selectin, and has a
XX CC high affinity for primary leukemia cells. The invention relates to
XX CC compositions utilising an agent and an antibody or its fragment. The
XX CC agent is a toxin, radioisotope or pharmaceutical agent such as
XX CC doxorubicin. It is complexed or combined with or conjugated to the
XX CC antibody or its fragment. The agent and/or antibody can be present in the
XX CC composition as a sub-clinical amount, i.e. less than the amount generally
XX CC found to be clinically effective when the agent is administered alone.
XX CC The composition is used in claimed methods of: inhibiting cell rolling,
XX CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
XX CC replication of tumor cells or leukemia cells, an increase in number of
XX CC tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,
XX CC platelet-platelet and/or cell-platelet complex formation, aggregation or
XX CC adhesion, increasing the mortality rate of tumor or leukemia cells, the
XX CC susceptibility of disease cells to damage by anti-disease agents, and the
XX CC susceptibility of tumor or leukemia cells to damage by anti-cancer
XX CC agents; and ameliorating the effects of a disease, preventing a disease,
XX CC treating a disease or inhibiting the progress of a disease.
XX CC
XX SQ Sequence 277 AA;
XX
XX Query Match 100.0%; Score 576; DB 8; Length 277;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-35;
XX Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDPRF 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 153 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDPRF 212
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTLTVLGA 111
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTLTVLGA 263
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XX
XX RESULT 14
XX ADI28367
XX ID ADI28367 standard; protein; 278 AA.
XX AC ADI28367;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX Human scfv fragment Y17, binds to platelets.
XX DE
```

```
XX OS Human; antibody; scfv; platelet; drug delivery; cancer; therapy.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX PA (SAVI-) SAVIENT PHARM INC.
XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX DR WPI; 2004-099189/10.
XX PT Composition comprising an agent and/or antibody or its fragment, useful
XX PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
XX PT for inhibiting growth and/or replication of tumor cells or leukemia
XX PT cells.
XX PS Claim 13; SEQ ID NO 2; 58pp; English.
XX CC The present sequence is the protein sequence of human scfv fragment Y17.
XX CC This antibody was identified by screening a human antibody phage library
XX CC that has diversity only in the heavy chain CDR3 regions. Fixed human
XX CC platelets were screened in order to identify antibodies that bind
XX CC platelets. Y17 binds leukemic cells. The invention relates to
XX CC compositions utilising an agent and an antibody or its fragment. The
XX CC agent is a toxin, radioisotope or pharmaceutical agent such as
XX CC doxorubicin. It is complexed or combined with or conjugated to the
XX CC antibody or its fragment. The agent and/or antibody can be present in the
XX CC composition as a sub-clinical amount, i.e. less than the amount generally
XX CC found to be clinically effective when the agent is administered alone.
XX CC The composition is used in claimed methods of: inhibiting cell rolling,
XX CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
XX CC replication of tumor cells or leukemia cells, an increase in number of
XX CC tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,
XX CC platelet-platelet and/or cell-platelet complex formation, aggregation or
XX CC adhesion, increasing the mortality rate of tumor or leukemia cells, the
XX CC susceptibility of disease cells to damage by anti-disease agents, and the
XX CC susceptibility of tumor or leukemia cells to damage by anti-cancer
XX CC agents; and ameliorating the effects of a disease, preventing a disease,
XX CC treating a disease or inhibiting the progress of a disease.
XX CC
XX SQ Sequence 278 AA;
XX
XX Query Match 100.0%; Score 576; DB 8; Length 278;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-35;
XX Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDPRF 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 154 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDPRF 213
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTLTVLGA 111
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 214 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGKTLTVLGA 264
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX
XX RESULT 15
XX AAB02186
XX ID AAB02186 standard; protein; 280 AA.
XX AC AAB02186;
XX XX
XX DT 10-AUG-2001 (first entry)
XX XX PAM2 single chain variable region (scfv) antibody.
XX DE
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Job time : 71.0521 secs

KM Pectin; PAM1 antibody; single chain variable region; scFv; food; jam;
 KM yogurt; gel; homogalacturonan; HG; plant cell wall.
 XX
 OS Unidentified.

Key	Location/Qualifiers
FT Peptide	1..22
FT	/label= pelB_leader_sequence
FT Region	23..138
FT	/label= Heavy_chain_fragment
FT Region	139..154
FT	/label= Linker
FT	155..275
FT Region	/label= Light_chain_fragment
FT	265..275
FT	/label= Myc_epitope
FT Misc-difference	279..80
FT	/note= "Encoded by TAGACT"

US6226599-B1.

08-MAY-2001.

26-FEB-1999; 99US-00260527.

24-DEC-1998; 98GB-00028700.

(DANI-) DANISCO AS.

Knox JP, Willats WGT, Mikkelsen JD;

WPI; 2001-342672/36.

N-PSDB; AAD06194.

PT New PAM1 and PAM2 antibodies capable of binding de-esterified
 PT homogalacturonan, useful for identifying a pectin moiety, for quantifying
 PT the amount of pectin in a sample or for extracting pectin from a sample.

PS Claim 2; Fig 4B; 21pp; English.

CC The invention relates to antibodies specific to pectin, such as PAM1 and
 CC PAM2 scFv (single chain variable region). These antibodies are derived
 CC from a naive phage display library known as the synthetic scFv library
 CC (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified
 CC and un-substituted homogalacturonan (HG), useful for identifying a pectin
 CC motif. PAM antibody is useful for identifying a pectin functional group
 CC and in assays to determine if a particular pectin composition has the
 CC pectin motif or can be used to prepare a food for human and animal
 CC consumption, such as jams, yogurts or gels. The PAM antibodies are
 CC further useful for quantifying the amount of pectin in a sample or for
 CC extracting pectin from a sample. PAM antibodies are also used to identify
 CC de-esterified homogalacturonan blocks in the primary cell walls of
 CC plants. The present sequence is PAM2 scFv antibody specific to pectin.
 CC Note: This sequence is stated as being the same as that shown as SEQ ID
 CC NO: 3 in the sequence listing of the specification, however the sequence
 CC has 2 extra residues at the C-terminal end

SQ Sequence 280 AA;

Query Match 100.0%; Score 576; DB 4; Length 280;
 Best Local Similarity 100.0%; Pred. No. 7e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDDPAVSAVAGQTVIRITCGDLSRSYASWYQKPGQAPVLIYIGKNNRPSGIPDRF 60
 DB 154 SELTDDPAVSAVAGQTVIRITCGDLSRSYASWYQKPGQAPVLIYIGKNNRPSGIPDRF 213

QY 61 SSSSGNTASTLTGAADEADYYCNSRDSGNNHVFSGGTCLTVLGAA 111
 DB 214 SSSSGNTASTLTGAADEADYYCNSRDSGNNHVFSGGTCLTVLGAA 264

Search completed: April 25, 2005, 20:22:17

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 49.1009 Seconds

(without alignments)
752.325 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576
Sequence: 1 SEITOPPAVVALGQTVRIT.....SGNHVFGGKTLVLGAAA 111Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
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- 9: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
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- 11: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
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- 17: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	15	US-10-032-037B-7
2	576	100.0	111	15	US-10-029-988B-7
3	576	100.0	111	15	US-10-032-423A-7
4	576	100.0	111	15	US-10-029-926B-7
5	576	100.0	125	17	US-10-888-959-8
6	576	100.0	266	15	US-10-032-037B-204
7	576	100.0	266	15	US-10-029-988B-204
8	576	100.0	266	15	US-10-032-423A-204
9	576	100.0	277	15	US-10-032-037B-25
10	576	100.0	277	15	US-10-032-037B-203
11	576	100.0	277	15	US-10-029-988B-25
12	576	100.0	277	15	US-10-029-988B-203
13	576	100.0	277	15	US-10-032-423A-25

14	576	100.0	277	15	US-10-032-423A-203	Sequence 203, App
15	576	100.0	277	15	US-10-029-926B-25	Sequence 25, App1
16	576	100.0	277	15	US-10-029-926B-203	Sequence 203, App1
17	576	100.0	280	17	US-10-880-922-5	Sequence 5, App1
18	576	100.0	280	17	US-10-880-922-6	Sequence 6, App1
19	576	100.0	280	17	US-10-880-922-55	Sequence 55, App1
20	576	100.0	280	17	US-10-880-922-56	Sequence 56, App1
21	576	100.0	280	17	US-10-880-922-60	Sequence 60, App1
22	576	100.0	280	17	US-10-880-922-61	Sequence 61, App1
23	576	100.0	309	13	US-10-050-798-9	Sequence 9, App1
24	576	100.0	309	14	US-10-288-917-9	Sequence 9, App1
25	576	100.0	309	15	US-10-423-448-9	Sequence 9, App1
26	576	100.0	312	13	US-10-052-798-10	Sequence 10, App1
27	576	100.0	312	14	US-10-288-917-10	Sequence 10, App1
28	576	100.0	312	15	US-10-423-448-10	Sequence 10, App1
29	564	97.9	153	10	US-09-988-115A-59	Sequence 59, App1
30	564	97.9	237	10	US-09-880-748-1941	Sequence 1941, App
31	564	97.9	237	10	US-09-880-748-2112	Sequence 2112, App
32	564	97.9	237	15	US-10-293-418-1941	Sequence 1941, App
33	564	97.9	237	15	US-10-293-418-2112	Sequence 2112, App
34	564	97.9	238	10	US-09-880-748-1907	Sequence 1907, App
35	564	97.9	238	15	US-10-293-418-1907	Sequence 1907, App
36	564	97.9	239	10	US-09-880-748-937	Sequence 937, App
37	564	97.9	239	10	US-09-880-748-2018	Sequence 2018, App
38	564	97.9	239	10	US-09-880-748-2038	Sequence 2038, App
39	564	97.9	239	15	US-10-293-418-937	Sequence 937, App
40	564	97.9	239	15	US-10-293-418-2018	Sequence 2018, App
41	564	97.9	239	15	US-10-293-418-2038	Sequence 2038, App
42	564	97.9	240	10	US-09-880-748-1912	Sequence 1912, App
43	564	97.9	240	10	US-09-880-748-1912	Sequence 1912, App
44	564	97.9	240	10	US-09-880-748-2013	Sequence 2013, App
45	564	97.9	240	14	US-10-322-672-52	Sequence 52, App1

ALIGNMENTS

RESULT 1
US-10-032-037B-7
; Sequence 7, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOLECULES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-7

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Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITOPPAVVALGQTVRITCGDLSRYASYOQKPGAPVLYYGNRRPSGIDRF 60
|||||
DB 1 SEITOPPAVVALGQTVRITCGDLSRYASYOQKPGAPVLYYGNRRPSGIDRF 60
|||||

QY 61 SGSSSGNTASLTITGAOAEDEADYYCNSRDSGNHVFSGGTJLVLGAAA 111
|||||
DB 61 SGSSSGNTASLTITGAOAEDEADYYCNSRDSGNHVFSGGTJLVLGAAA 111
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RESULT 2
US-10-029-988B-7

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; Sequence 7, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-7
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Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
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US-10-032-423A-7
; Sequence 7, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-7
```

```
Query Match          100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SELTOPPAVSVALGQTVRITTCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 1 SELTOPPAVSVALGQTVRITTCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
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RESULT 4
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; Sequence 7, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAANY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
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; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-7
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Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 SELTOPPAVSVALGQTVRITTCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
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RESULT 5
US-10-888-959-8
; Sequence 8, Application US/10888959
; Publication No. US20050048545A1
; GENERAL INFORMATION:
; APPLICANT: Cull, Millard
; APPLICANT: Brennan, Miles
; APPLICANT: Gill, Ronald
; TITLE OF INVENTION: Universal Detection of Binding
; FILE REFERENCE: BPP.03
; CURRENT APPLICATION NUMBER: US/10/888,959
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/487,018
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/509,196
; PRIOR FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: variable light chain domain
US-10-888-959-8
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Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 SELTOPPAVSVALGQTVRITTCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
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RESULT 6
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: MOIETTES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
```

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/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032.037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-037B-204

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DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGGTXTLVGAAA 111

RESULT 7
US-10-029-988B-204
/ Sequence 204, Application US/10029988B
/ Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029.988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-029-988B-204

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Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGGTXTLVGAAA 111

RESULT 8
US-10-032-423A-204
/ Sequence 204, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032.423A
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
```

```
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match          100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGGTXTLVGAAA 111

RESULT 9
US-10-032-037B-25
/ Sequence 25, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032.037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGGTXTLVGAAA 263

RESULT 10
US-10-032-037B-203
/ Sequence 203, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032.037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 203
/ LENGTH: 277
/ TYPE: PRF
```

```
; ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
    |||
DB 153 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 111
    |||
DB 213 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 263

RESULT 11
US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
    |||
DB 153 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 111
    |||
DB 213 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 263

RESULT 12
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
```

```
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
    |||
DB 153 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 111
    |||
DB 213 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 263

RESULT 13
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
    |||
DB 153 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 111
    |||
DB 213 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTTLTVLGAAA 263

RESULT 14
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
    |||
DB 153 SEITDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
```


Qy 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 111
 |||||
 Db 213 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 263

RESULT 15
 US-10-029-926B-25
 ; Sequence 25, Application US/10029926B
 ; Publication No. US20040073011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HAGAY, et al.
 ; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
 ; FILE REFERENCE: 10793/50
 ; CURRENT APPLICATION NUMBER: US/10/029, 926B
 ; PRIOR FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: 60/258,948
 ; PRIOR FILING DATE: 12/29/2000
 ; NUMBER OF SEQ ID NOS: 203
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 277
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-029-926B-25

Query Match 100.0%; Score 576; DB 15; Length 277;
 Best Local Similarity 100.0%; Pred. No. 8e-44;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTOPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYIYGKNNRPSGIPDRF 60
 |||||
 Db 153 SELTOPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYIYGKNNRPSGIPDRF 212
 |||||
 Qy 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 111
 |||||
 Db 213 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 263

Search completed: April 25, 2005, 21:09:46
 Job time : 50.1009 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: April 25, 2005, 19:57:16 ; Search time 12.7982 Seconds
(without alignments)
834.495 Million cell updates/sec

Title: US-10-029-926d-7

Sequence: 1 SEITDPAVVALGQTVRIT.....SGNHVFGGKTLTVGAAA 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	97.9	109	2	SI9663
2	558	96.9	108	2	S47184
3	547.5	95.1	110	2	S36272
4	542	94.1	127	2	S70444
5	541	93.9	108	2	S38498
6	535	92.9	109	2	S38496
7	527	91.5	108	1	L3HUSH
8	526	91.3	233	2	S25748
9	517.5	89.8	146	2	S02083
10	514.5	89.3	110	2	S19672
11	499	86.6	96	2	S36060
12	499	86.6	115	2	S13726
13	488	86.5	233	2	S25741
14	438.5	76.1	106	2	S38493
15	420	72.9	105	2	S49533
16	414	71.9	190	2	S25740
17	410	71.2	119	2	S30526
18	397	68.9	107	2	PC4823
19	395.5	68.7	120	2	S30525
20	384	66.7	226	2	S25745
21	381	66.1	231	2	S25751
22	376	65.3	120	2	S25738
23	376	65.3	120	2	S25739
24	376	65.3	151	2	S25737
25	376	65.3	231	2	S25753
26	374	64.9	233	2	S25747
27	373.5	64.8	212	2	S70431
28	370	64.2	107	1	L4H0HL
29	370	64.2	108	1	L5H0DL

30	369	64.1	106	1	L4H0BU	Ig lambda chain V-
31	367	63.7	132	2	S09713	Ig lambda chain V
32	365.5	63.5	112	2	S51148	Ig lambda chain V
33	363.5	63.1	232	2	S25756	Ig lambda chain -
34	362	62.8	106	1	L4H0ML	Ig lambda chain V-
35	358	62.2	106	1	L4H0X	Ig lambda chain V-
36	355	61.6	109	2	S68171	Ig lambda chain V
37	353	61.3	111	2	S36274	Ig lambda chain V
38	353	61.3	128	2	S24319	Ig lambda chain pr
39	346	60.1	105	2	S44124	Ig lambda chain pr
40	344	59.7	225	2	S05270	Ig lambda chain pr
41	343	59.5	111	2	S47009	Ig lambda chain V1
42	342	59.4	111	1	L2H0MC	Ig lambda chain V-
43	341	59.2	95	2	S36065	Ig lambda chain -
44	341	59.2	114	2	S16440	Ig lambda chain -
45	340	59.0	106	1	L4H0XN	Ig lambda chain V-

ALIGNMENTS

RESULT 1

SI9663
Ig lambda chain V region (clone alpha-BSA3) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: SI9663
R:Mark: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Grifflths, A.D.; Winter
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p
A:Reference number: SI9663; PMID:92085276; PMID:1748994
A:Accession: SI9663
A:Molecule type: mRNA
A:Residues: 1109 <MAN>
A:Cross-references: EMBL:X61640; NID:G29492; PIDN:CAA3821.1; PID:G1340166
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 97.9%; Score 564; DB 2; Length 109;
Matches 108; Conservative 100.0%; Pred. No. 1.8e-41; Indels 0; Gaps 0;

QY 1 SEITDPAVVALGQTVRITCOGDSLSRYASRYOQKPGAPVLYTKNNRPSGIFDRF 60
DB 2 SEITDPAVVALGQTVRITCOGDSLSRYASRYOQKPGAPVLYTKNNRPSGIFDRF 61

QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFSGGKTLTVLG 108
DB 62 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFSGGKTLTVLG 109

RESULT 2

S47184

Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47184

R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994

A:Description: Cloning and analysis of Igm anti-thyroglobulin autoantibodies from patient

A:Reference number: S47181

A:Accession: S47184

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <MCi>

A:Cross-references: EMBL:X79783; NID:G506426; PIDN:CAA56179.1; PID:G506427

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-89/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 96.9%; Score 558; DB 2; Length 108;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 60

Db 2 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 107

Db 62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 108

RESULT 3

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C/Accession: S36272

R/Griffiths, A.D.; Malingvalst, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MUID:9318448; PMID:7679990

A/Accession: S36272

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-110 <GRI>

A/Cross-references: EMBL:Z18833; NID:G33419; PIDN:CAA79285.1; PID:G939912

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 95.1%; Score 547.5; DB 2; Length 110;

Best Local Similarity 98.2%; Pred. No. 4.6e-40;

Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 60

Db 2 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 108

Db 62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 110

RESULT 4

S70444

Ig lambda chain precursor V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: S70444; S70426

R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.

Mol. Immunol. 29, 1363-1373, 1992

A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of B

A/Reference number: S70442; MUID:93024508; PMID:1383695

A/Accession: S70444

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-127 <CUI>

A/Cross-references: UNIPROT:Q9NSDS

A/Experimental source: Clone E29.1

R/Tonnelie, C.

submitted to the EMBL Data Library, May 1990

A/Accession: S70426

A/Molecule type: mRNA

A/Residues: 1-90 <TON>

A/Cross-references: EMBL:X53070

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/20/Domain: signal sequence #status predicted <SIG>

F/21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>

F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 94.1%; Score 542; DB 2; Length 127;

Best Local Similarity 97.2%; Pred. No. 1.6e-39;

Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 60

Db 21 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 80

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 107

Db 81 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 127

RESULT 5

S38498

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S38498

R/Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, J.

submitted to the EMBL Data Library, June 1993

A/Description: Human antibody fragments specific for human blood group antigens from a

A/Reference number: S38488

A/Accession: S38498

A/Status: preliminary

A/Molecule type: DNA

A/Cross-references: EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; PID:G414044

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/14-88/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 541; DB 2; Length 108;

Best Local Similarity 97.2%; Pred. No. 1.6e-39;

Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 60

Db 1 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 60

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 108

Db 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 108

RESULT 6

S38496

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S38496

R/Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, J.

submitted to the EMBL Data Library, June 1993

A/Description: Human antibody fragments specific for human blood group antigens from a

A/Reference number: S38488

A/Accession: S38496

A/Status: preliminary

A/Molecule type: DNA

A/Cross-references: EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PID:G414040

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 535; DB 2; Length 109;

Best Local Similarity 93.5%; Pred. No. 5.3e-39;

Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 60

Db 2 SEITODPAVSVALGQVTRITTCQDLSRSYYASWYQOKPGQAPVLYVYGGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 108

Db 62 SGGSPNTASLTITGAQAEDEADYYCTSRDTSRGNHVFEGGKTLTVLG 109

RESULT 7

L3HUSH

Ig lambda chain V-III region (Sh) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C/Accession: A01980

R/Title: K.; Wikler, M.; Shinoda, T.; Putnam, F.W.

J. Biol. Chem. 245, 2171-2176, 1970

A/Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete

A/Reference number: A92057; PMID:7016723; PMID:4909564

A/Accession: A01980

A/Molecule type: protein

A/Residues: 1-108 <TIT>

A/Cross-references: UNIPROT:P01714

A/Note: the sequence of the C region is also given

C/Genetics:

A/Genes: GDB:IGLV6

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/14-88/Domain: immunoglobulin homology <IMM>

F/21-86/Disulfide bonds: #status experimental

Query Match 91.5%; Score 527; DB 1; Length 108;

Best Local Similarity 92.6%; Pred. No. 2.6e-38;

Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SETTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60

Db 1 SETTOPPAVSVALGQTVRITCGDLSRFGYDAWYQKPGQAPLVITYGKNNRPSGIPDRF 60

QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVLG 108

Db 61 SSSSGHTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVLG 108

RESULT 8

S25748

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S25748

R/Combrlato, G.; Kloebeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lam

A/Reference number: S16439; PMID:91257162; PMID:1904362

A/Accession: S25748

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-233 <COM>

A/Cross-references: EMBL:X57813; NID:G33725; PTDN:CAA40950.1; PID:G33726

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/148-216/Domain: immunoglobulin homology <IMM>

Query Match 91.3%; Score 526; DB 2; Length 233;

Best Local Similarity 91.7%; Pred. No. 6.6e-38;

Matches 99; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 SETTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60

Db 21 SETTOPPAVSVALGQTVRITCGDLSRATYASWYQKPGQAPLVITYGKNNRPSGIPDRF 80

QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVLG 108

Db 81 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVLG 128

RESULT 9

S02083

Ig lambda chain V-IV region - human (tentative sequence) (fragments)

N/Alternate names: amyloid-fibril protein GIL

C/Species: Homo sapiens (man)

C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000

C/Accession: S02083

R/PKase, E.M.; Sletten, K.; Hueb, G.; Cornwell III, G.G.

Biochem. J. 256, 973-980, 1988

A/Title: The primary structure of the variable region of an immunoglobulin IV light-cha

A/Reference number: S02083; PMID:89134210; PMID:3146581

A/Accession: S02083

A/Molecule type: protein

A/Residues: 1-70; 71-72; 73-75; 76-131; 132-146 <FK>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/14-88/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 517.5; DB 2; Length 146;

Best Local Similarity 91.7%; Pred. No. 2.2e-37;

Matches 99; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

QY 1 SETTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60

Db 1 SETTOPPAVSVALGQTVRITCGDLSRNFASWYQKPGQAPLVITYGKNNRPSGIPDRF 60

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVL 107

Db 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVL 108

RESULT 10

S19672

Ig lambda chain V region (clone alpha-TEU14) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19672

R/Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p

A/Reference number: S19673; PMID:92085276; PMID:1748994

A/Accession: S19672

A/Molecule type: mRNA

A/Residues: 1-110 <MAR>

A/Cross-references: EMBL:X61644; NID:G37856; PTDN:CAA43825.1; PID:G1335384

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 514.5; DB 2; Length 110;

Best Local Similarity 91.7%; Pred. No. 3e-37;

Matches 100; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 SETTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60

Db 2 SETTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVLG 108

Db 62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGKTLTVLG 110

RESULT 11

S36060

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

R/Williams, S.C.

submitted to the EMBL Data Library, April 1993

A/Reference number: S36046

A/Accession: S36060
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-96 <NLS>
A/Cross-references: EMBL:Z22202; NID:g312325; PIDN:CAA80211.1; PID:g312326
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 499; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.6e-36;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60
|||
2 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 61

DB 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 95
|||
62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 96

RESULT 12

S13726

Ig lambda chain V region - human

C/Species: Homo sapiens (man)

C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S13726

R:Ripplac, J.P.; Chuchana, P.; Bernard, F.; Bulwela, L.; Lefranc, G.; Lefranc, M.P.

Nucleic Acids Res. 18, 7134, 1990

A/Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup

A/Reference number: S13726; MUID:91088295; PMID:2124677

A/Accession: S13726

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-115 <PRI>

A/Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405

C/Genetics:

A/Intons: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 499; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60
|||
21 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 80

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 95
|||
81 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 115

RESULT 13

S25741

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S25741

R:Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lam

A/Reference number: S16439; MUID:91257162; PMID:1904362

A/Accession: S25741

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-233 <COM>

A/Cross-references: EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 498; DB 2; Length 233;
Best Local Similarity 86.9%; Pred. No. 1.6e-35;
Matches 93; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60
|||
21 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 80

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLTTL 107
|||
81 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLTTL 127

RESULT 14

S38495

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S38495

R:Waks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finern, R.; Gorick, B.D.; Voak, D.; Thorpe, L.

Submitted to the EMBL Data Library, June 1993

A/Description: Human antibody fragments specific for human blood group antigens from a

A/Reference number: S38488

A/Accession: S38495

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-106 <MAR>

A/Cross-references: EMBL:Z23029; NID:g414037; PIDN:CAA80564.1; PID:g414038

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 438.5; DB 2; Length 106;
Best Local Similarity 78.7%; Pred. No. 8.9e-31;
Matches 85; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 1 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60
|||
2 SEITOPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLTTL 108
|||
62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGKTLTTL 106

RESULT 15

S49533

anti-5m antibody VL chain (V lambda 3b/J lambda 2/3) - human

C/Species: Homo sapiens (man)

C/Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000

C/Accession: S49533

R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

Submitted to the EMBL Data Library, October 1994

A/Description: Molecular characterization of natural human anti-5m autoantibodies.

A/Reference number: S48797

A/Accession: S49533

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-105 <MAH>

A/Cross-references: EMBL:Z46346; NID:g560845; PIDN:CAA86465.1; PID:g1340169

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 420; DB 2; Length 105;
Best Local Similarity 76.2%; Pred. No. 3.4e-29;
Matches 80; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 TOPPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRFSGS 63
|||
1 TOPPAVSVALGQTVRTTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRFSGS 60

Qy 64 SSGNTASLTTTGAQAEDEADYCNRSRDSGNHVPFGGTXLTVLG 108
Db 61 SSGTIVTLTFTISGVQAEDEADYCSADSSGTYVVPFGGTXLTVLG 105

Search completed: April 25, 2005, 20:24:06
Job time : 13.7982 secs

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RT Titani K., Wixler M., Shinoda T., Putnam F.W.;
RA "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
bridges."
RL J. Biol. Chem. 245:2171-2176(1970).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR, A01980; L3HUSH.
DR HSSP, P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 97 Ig-like.
FT DISULFID 21 86
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 91.5%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 1,6e-44;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SETTOPPAVSVALGQVVRITTCGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRF 60
DB 1 SETTOPPAVSVALGQVVRITTCGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRF 60
DB 1 SETTOPPAVSVALGQVVRITTCGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTLYTLG 108
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTLYTLG 108
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTLYTLG 108

RESULT 3
Q6GMW4 PRELIMINARY; PRT; 233 AA.
AC 06GMW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.B.,

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC073786; AAH73786.1; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR006662; Thiolred.
DR Pfam; PF07654; C1-sec; 1.
DR Pfam; PF00047; Ig; 2.
DR PRINTS; PR00421; THIOREDOXIN.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypoetical protein.
SQ SEQUENCE 233 AA; 24855 MW; 462677B3B8DE5BD CRC64;

Query Match 91.3%; Score 526; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 4,8e-44;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 SETTOPPAVSVALGQVVRITTCGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRF 60
DB 21 SETTOPPAVSVALGQVVRITTCGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRF 80
DB 21 SETTOPPAVSVALGQVVRITTCGDSLRSYYASWYQOKPGQAPLVLYGKNNRPSGIPDRF 80
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTLYTLG 108
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTLYTLG 108
DB 81 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTLYTLG 128

RESULT 4
Q8TBC9 PRELIMINARY; PRT; 233 AA.
AC 08TBC9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C.,

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RA Krzywinski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RU Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028283; AAH28283.1; -.
DR PIR; S12442; S12442.
DR PIR; S30525; S30525.
DR PIR; S30526; S30526.
DR HSSP; P01842; 1LIL.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 74.1%; Score 427; DB 2; Length 233;
Best Local Similarity 76.8%; Pred. No. 3.2e-34;
Matches 82; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELTQDPAVSVALGQTVRITCGDLSRSYASWTQKPGAPVLYIGKNNRPSGIDPRFS 61
DB 22 ELTQPSVSVPQGTARITCGDALPKQYVWYQKRGAPVLYIGKNNRPSGIDPRFS 81
QY 62 GSSSGTASITJTGADQEDADYVNSRDSSGNHVVFGGCTKTTLTG 108
DB 82 GSSSGTAVTLTIGVQADEADYVNSRDSSGTYWVGCGTKTLTLG 128

RESULT 5
Q722E8 PRELIMINARY; PRT; 81 AA.
AC Q722E8;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Rearranged VJ31 segment (Rearranged VJ31 gene segment)
DE (Fragment).
GN Name=VJ31;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin Lymphoma, and Mantle cell Lymphoma;
RA Tingirely M., Rosenquist R., Sundstrom C., Amin R.M., Koppers R.,
RA Handmann M.U., Brauning A.;
RU Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564423; CAD92030.1; -.
DR EMBL; AJ564424; CAD92031.1; -.
DR HSSP; P01709; 1DCL.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 81 AA; 8702 MW; CFF1D466B794C9F CRC64;

Query Match 73.3%; Score 422; DB 2; Length 81;
Best Local Similarity 96.3%; Pred. No. 3.1e-34;
Matches 78; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 19 ITTCGDSLSRSYASWTQKPGAPVLYIGKNNRPSGIDPRFGSSSGNTASITITGAQA 78
DB 1 ITTCGDSLSRSFYASWTQKPGAPVLYIGKNNRPSGIDPRFGSSSGNTASITITGAQA 60
QY 79 EDEADYVNSRDSSGNHVVFG 99
DB 61 EDEADYVNSRDSSGNHVVFG 81

RESULT 6
Q8NSF4 PRELIMINARY; PRT; 233 AA.
ID Q8NSF4;
AC Q8NSF4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulian S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RU Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032452; AAH32452.1; -.
DR PIR; A39949; A39949.
DR PIR; S12441; S12441.
DR PIR; S12443; S12443.
DR HSSP; P01842; 1LIL.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6A6E3A9A CRC64;

Query Match 72.2%; Score 416; DB 2; Length 233;
Best Local Similarity 74.8%; Pred. No. 3.9e-33;
Matches 80; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

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Db 22 ELTOPSVSVSGPQTARITCGDAPLPRKAYWYQKSGQTPVLVIYDTERPSGIPERS 81
QY 62 GSSSGNTATLTITGAQAEDEADYYCNSRDSGNHVFGGGTKLTVLG 108
Db 82 GSSSGVTATLTLSGAQVEDEADYYCNSRDSGNHVFGGGTKLTVLG 128

RESULT 7
ID 08N355 PRELIMINARY; PRT; 234 AA.
AC 08N355;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypochemical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RX Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028090; AAH28090.1; -.
DR PIR; S09713; S09713.
DR PIR; S12441; S12441.
DR PIR; S30527; S30527.
DR HSSP; P01842; 1LIL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypochemical protein.
SQ SEQUENCE 234 AA; 24792 MW; CC848CABA9A9D63 CRC64;

Query Match 65.9%; Score 379.5; DB 2; Length 234;
Best Local Similarity 70.1%; Pred. No. 1.3e-29;
Matches 75; Conservative 12; Mismatches 19; Indels 1; Gaps 1;
QY 3 LTODPAVVALGQTVRTTCQGSLSRSYYASWYQKPGQAVLYIYGNKRRPSGIPDRFSG 62
Db 23 LTQPPSVSVAPGQTARITCGDAPLPRKAYWYQKSGQTPVLVIYDTERPSGIPERS 82
QY 63 SSSSGNTATLTITGAQAEDEADYYCNSRDSGNH-VVFGGTKLTVLG 108

Db 83 SNSGNTATLTISRVDAGDEADYYCOLMSSSDHPVVFGGGTKLTVLG 129

RESULT 8
ID LV3B_HUMAN STANDARD; PRT; 111 AA.
AC P80748;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Ig lambda chain V-II region LOI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
RC TISSUE=Urine;
RX MEDLINE=99441384; PubMed=10510403;
RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
RT "Nephriticogenic lambda light chain dimer: a unique human
miniautoantibody against complement factor H.";
RL J. Immunol. 163:4590-4596(1999).
CC -1- FUNCTION: Activates the alternative complement pathway by binding
to the short consensus repeat domain 3 (SCR3) of factor H.
CC -1- SUBUNIT: Homodimer.
CC -1- DISEASE: The blocking of factor H by LOI protein leads to the
developmental of membranoproliferative glomerulonephritis (MPGN).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PDB; 2DOI; Model; A/B=1-11.
DR GO; GO:0005976; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF0047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 97
FT SITE 48 51 SCR3 binding.
FT BINDING 15 15 SCR3.
FT BINDING 25 25 SCR3.
FT BINDING 29 29 SCR3.
FT BINDING 94 94 SCR3.
FT DISULFID 21 86 By similarity.
FT STRAND 4 8
FT STRAND 8 8
FT TURN 13 14
FT STRAND 16 22
FT STRAND 32 37
FT TURN 38 40
FT STRAND 41 46
FT TURN 49 50
FT STRAND 54 54
FT TURN 55 55
FT TURN 58 59
FT STRAND 60 61
FT STRAND 64 65
FT TURN 66 67
FT STRAND 68 74
FT TURN 78 79
FT STRAND 82 88
FT TURN 91 93
FT STRAND 97 98
FT STRAND 102 104
FT TURN 107 108
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11935 MW; 69498BEBFDE82053 CRC64;
Query Match 65.5%; Score 377; DB 1; Length 111;
Best Local Similarity 69.5%; Pred. No. 1.3e-29;

Query Match	Best Local Similarity	64.1%	Score 369.5	DB 2	Length 107
Matches 74	Conservative	8	Mismatches 23	Indels 1	Gaps 1
Qy	2 ELTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAPLVLYTGKNNRPSGIPDRFS	61			
Db	3 ELTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAPLVLYTGKNNRPSGIPDRFS	62			
Qy	62 GSSSGNTASLTITGQAQDEADYDNCNSDSSGNHVFEGGKTLTVL	107			
Db	63 GSSSGNTASLTITGQAQDEADYDNCNSDSSGNHVFEGGKTLTVL	107			
RESULT 12					
Qy	1V4A_HUMAN	STANDARD	PRT	106 AA	
Db	1V4A_HUMAN	STANDARD	PRT	106 AA	
Qy	62 GSSSGNTASLTITGQAQDEADYDNCNSDSSGNHVFEGGKTLTVL	107			
Db	63 GSSSGNTASLTITGQAQDEADYDNCNSDSSGNHVFEGGKTLTVL	107			
RESULT 13					
Qy	1V4E_HUMAN	STANDARD	PRT	106 AA	
Db	1V4E_HUMAN	STANDARD	PRT	106 AA	
Qy	62 GSSSGNTASLTITGQAQDEADYDNCNSDSSGNHVFEGGKTLTVL	107			
Db	63 GSSSGNTASLTITGQAQDEADYDNCNSDSSGNHVFEGGKTLTVL	107			

[illegible]

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravinsky M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073769; AAH73769.1; --
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein.
 KM SEQUENCE 236 AA; 24809 MW; BA0AF0F4192364A5 CRC64;
 SQ

Query Match 62.6%; Score 360.5; DB 2; Length 236;
 Best Local Similarity 66.7%; Pred. No. 1.3e-27;
 Matches 74; Conservative 8; Mismatches 26; Indels 3; Gaps 1;
 QY 1 SEITDPAYVALGQTVRITTCGDSLR--SYTASVYQKPGQAPVLYIGKNNRPSGIP 57
 DB 21 SVLTQPPVSVAAGPQRTVTSCTSSSNIGAGYDVHWQQLPGLTAPRLILYGNRNRPSPGVP 80
 QY 58 DRESGSSSGNTATLTITGAQAEDEADYVYCNRRDSSGNHVFEGGKTLTVL 108
 DB 81 DRFGSKSGTSSALITGLQAEDEADYVYCNRRDSSGNHVFEGGKTLTVL 131

RESULT 15
 Q6NS96 PRELIMINARY; PRT; 233 AA.
 ID 06NS96;
 AC 06NS96;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heide F.,
 RA Diatchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Kravinsky M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC070352; AAH70352.1; --
 DR HSSP; P01709; IABU.
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein.
 KM SEQUENCE 233 AA; 24899 MW; D3B0A54F2972D473 CRC64;
 SQ

Query Match 62.5%; Score 360; DB 2; Length 233;
 Best Local Similarity 64.8%; Pred. No. 1.4e-27;
 Matches 68; Conservative 16; Mismatches 21; Indels 0; Gaps 0;
 QY 3 LTODPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLYIGKNNRPSGIPDFSG 62
 DB 23 LTQPPVSVAAGPQRTVTSCTSSSNIGAGYDVHWQQLPGLTAPRLILYGNRNRPSPGVP 80
 QY 63 SSSGNTATLTITGAQAEDEADYVYCNRRDSSGNHVFEGGKTLTVL 107
 DB 83 SNGGNTATLTITSRVAGDEADYVYCNRRDSSGNHVFEGGKTLTVL 127

Search completed: April 25, 2005, 20:33:56
 Job time : 59.3459 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 169.824 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926d-25

Perfect score: 1440

Sequence: 1 MKVLPPTAAAGLLLAQPA.....VLGAABEQKLISEEDLNGAA 277

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1440	100.0	277	5	ABG78150 Human Fv
2	1440	100.0	277	5	ABG91841 Human ant
3	1436	99.7	277	8	AD128366 Human scf
4	1416	98.3	277	5	ABG78328 Human Fv
5	1416	98.3	277	5	ABG92019 Human ant
6	1397.5	97.0	278	8	AD128367 Human scf
7	1393.5	96.8	280	8	ADJ57363 P-selecti
8	1386.5	96.3	280	8	AD128368 Human scf
9	1378	95.7	266	5	ABG92020 Human ant
10	1294	89.9	291	8	ADN06989 Human Bfg
11	1278.5	88.8	282	4	AAE02185 Human Fv
12	1275.5	88.6	309	2	AAW83322 Single ch
13	1275.5	88.6	309	5	ABW09603 Amino aci
14	1275.5	88.6	309	6	ABG74384 Single ch
15	1275.5	88.6	309	7	ADG98737 Human sin
16	1275.5	88.6	309	8	AD040446 Human sin
17	1257	87.3	246	5	ABG78329 Human Fv
18	1257	87.3	246	5	ABG92026 Antibody
19	1250	86.8	256	5	ABG78334 Human Fv
20	1250	86.8	256	5	ABG92025 Antibody
21	1231.5	85.5	260	5	ABG92023 Antibody
22	1223	84.9	263	5	ABG92024 Antibody
23	1218.5	84.6	239	7	ADG95753 Human Bly
24	1218.5	84.6	239	7	ADG95753 Single ch
25	1212.5	84.2	239	5	ABP46027 Human Bly

26	1212.5	84.2	239	7	ADG96854
27	1201.5	83.4	290	6	ABP55318
28	1201.5	83.4	290	7	AD199518
29	1194	82.9	312	2	AAW83323
30	1194	82.9	312	5	ABW09604
31	1194	82.9	312	6	ABG74385
32	1194	82.9	312	7	ADG98738
33	1194	82.9	312	8	AD040447
34	1191.5	82.7	239	5	ABP46004
35	1191.5	82.7	239	7	ADG96831
36	1191	82.7	291	5	AAE29202
37	1188.5	82.5	296	5	ABG60637
38	1188.5	82.5	296	7	AD199519
39	1186	82.4	291	5	ABG60632
40	1181	82.0	238	3	AAW95198
41	1178	81.8	244	6	AAO31136
42	1149	79.8	242	8	AD158068
43	1139.5	79.1	239	5	ABP46007
44	1139.5	79.1	239	7	ADG96834
45	1133	78.7	244	6	AAO31139

ALIGNMENTS

RESULT 1
ABG78150
ID ABG78150 standard; protein; 277 AA.

AC ABG78150;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

PN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

PR 29-DEC-2000; 2000US-00751181.

XX (BIOR-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarevits J, Guy R, Lipschitz O, Stanton E, Levanon A;

PI Plakain D, Peretz T;

DR WPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

PT characteristice so as to selectively bind target cell in favor of other

PS Claim 4; Page 155-156; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv

CC molecule, a construct or fragments or a construct of a fragment with

CC enhanced binding characteristics which selectively and/or specifically

CC binds to a target cell in favour of other cells, where binding is

CC primarily determined by a first hypervariable region and Fv is a single

CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX

SQ Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 4,5e-89;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRGSLRLSCAASGFTFDDYGMYSWR 60
DB 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRGSLRLSCAASGFTFDDYGMYSWR 60
QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNKNSLYIQNNSLRAEDTAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNKNSLYIQNNSLRAEDTAVYYCAR 120
QY 121 MRAPVIMGGTTLTVSRGGSGGGSGGSELTPDPAVSVVALGQTVRITCGDLSLR 180
DB 121 MRAPVIMGGTTLTVSRGGSGGGSGGSELTPDPAVSVVALGQTVRITCGDLSLR 180
QY 181 YVASWYQOKRGPAPVLYVYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YVASWYQOKRGPAPVLYVYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
QY 241 RDSSGNHVVFGGGTLTVLGAABEQKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGGTLTVLGAABEQKLISEEDLNGAA 277

RESULT 2

ABG91841
ID ABG91841 standard; protein; 277 AA.

XX AC ABG91841;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #25.

XX KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX KM metastasis; hypervariable region; autoimmune disease; thrombosis;
XX KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX KM myocardial infarction; retinopathic disease; abnormal platelet function;
XX KM sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN W0200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX PI Sanchon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX DR WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in
XX PT physiological phenomena such as cell rolling, metastasis and
XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX PT diseases, and cancer.

XX PS Claim 23; Page 233-234; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention

SQ Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 4,5e-89;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRGSLRLSCAASGFTFDDYGMYSWR 60
DB 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRGSLRLSCAASGFTFDDYGMYSWR 60
QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNKNSLYIQNNSLRAEDTAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNKNSLYIQNNSLRAEDTAVYYCAR 120
QY 121 MRAPVIMGGTTLTVSRGGSGGGSGGSELTPDPAVSVVALGQTVRITCGDLSLR 180
DB 121 MRAPVIMGGTTLTVSRGGSGGGSGGSELTPDPAVSVVALGQTVRITCGDLSLR 180
QY 181 YVASWYQOKRGPAPVLYVYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YVASWYQOKRGPAPVLYVYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
QY 241 RDSSGNHVVFGGGTLTVLGAABEQKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGGTLTVLGAABEQKLISEEDLNGAA 277

RESULT 3

AD128366
ID AD128366 standard; protein; 277 AA.

XX AC AD128366;

XX DT 06-MAY-2004 (first entry)

XX DE Human scFv fragment YL, binds to platelets.

XX KM Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

XX OS Homo sapiens.

XX PN W02004002528-A1.

XX PD 08-JAN-2004.

XX PF 30-JUN-2003; 2003WO-US020604.

XX PR 01-JUL-2002; 2002US-00189025.

XX PA (SAVI-) SAVIENT PHARM INC.

XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX WPI; 2004-099189/10.
XX
XX Composition comprising an agent and/or antibody or its fragment, useful
XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or
XX for inhibiting growth and/or replication of tumor cells or leukemia
XX cells.
XX
XX Claim 13; SEQ ID NO 1, 58pp; English.
XX
XX The present sequence is the protein sequence of human scFv fragment Y1.
XX This antibody was identified by screening a human antibody phage library
XX that has diversity only in the heavy chain CDR3 regions. Fixed human
XX platelets were screened in order to identify antibodies that bind
XX platelets. The epitope for Y1 antibody is located between amino acids 272
XX and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the
XX N-terminal of PEG-1, a receptor for E-, L- and P-selectins, and has a
XX high affinity for primary leukemia cells. The invention relates to
XX compositions utilising an agent and an antibody or its fragment. The
XX agent is a toxin, radioisotope or pharmaceutical agent such as
XX doxorubicin. It is complexed or combined with or conjugated to the
XX antibody or its fragment. The agent and/or antibody can be present in the
XX composition is a sub-clinical amount, i.e. less than the amount generally
XX found to be clinically effective when the agent is administered alone.
XX The composition is used in claimed methods of: inhibiting cell rolling,
XX inflammation, thrombosis, restenosis, metastasis, the growth and/or
XX replication of tumor cells or leukemia cells, an increase in number of
XX tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,
XX platelet-platelet and/or cell-platelet complex formation, aggregation or
XX adhesion; increasing the mortality rate of tumor or leukemia cells, the
XX susceptibility of disease cells to damage by anti-disease agents, and the
XX agents; and ameliorating the effects of a disease, preventing a disease,
XX treating a disease or inhibiting the progress of a disease.
XX
XX Sequence 277 AA;
SQ
Query Match 99.7%; Score 1436; DB 8; Length 277;
Best Local Similarity 99.6%; Pred. No. 8.4e-89;
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVRRPGSLRLSCAAGFTFDDYGMWVR 60
DB 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVRRPGSLRLSCAAGFTFDDYGMWVR 60
QY 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAR 120
QY 121 MRAPVIMGGQTLTVTSRGGSGGGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180
DB 121 MRAPVIMGGQTLTVTSRGGSGGGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180
QY 181 YVASWYQOKRPGQAPVLYVIGKNNRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240
DB 181 YVASWYQOKRPGQAPVLYVIGKNNRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240
QY 241 RDSSGNHVVFGGCTKLTIVGAAAEOKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGCTKLTIVGAAAEOKLISEEDLNGAA 277
RESULT 4
ABG78328
XX ABG78328 standard; protein; 277 AA.
XX
XX ABG78328;
AC
XX
XX 15-NOV-2002 (first entry)
XX
XX Human Fv molecule hypervariable region related peptide #203.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;
XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.
XX
XX Homo sapiens.
XX
XX WO200259264-A2.
XX
XX 01-AUG-2002.
XX
XX 31-DEC-2001; 2001WO-US049440.
XX
XX 29-DEC-2000; 2000US-00751181.
XX
XX (BIO-) BIO-TECHNOLOGY GEN CORP.
XX
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
XX Plakshin D, Peretz T;
XX
XX WPI; 2002-619166/66.
XX N-PSDB; ABS63384.
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX or fragment, or construct of fragment with enhanced binding
XX characteristic so as to selectively bind target cell in favor of other
XX cells.
XX
XX Claim 14; Fig 14; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
XX molecule, a construct or fragments or a construct of a fragment with
XX enhanced binding characteristics which selectively and/or specifically
XX binds to a target cell in favour of other cells, where binding is
XX primarily determined by a first hypervariable region and Fv is a single
XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX association with or attached, coupled, combined, linked or fused to a
XX pharmaceutical agent, is useful in the manufacture of a medicament, where
XX the medicament has activity against a diseased cell, preferably a cancer
XX cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
XX myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
XX acute myeloid leukemia cell). The peptide is also useful for preparing a
XX composition for use in inhibiting the growth of a diseased or cancer
XX cell. This sequence represents a human Fv molecule hypervariable region
XX related peptide of the invention
XX
XX Sequence 277 AA;
SQ
Query Match 98.3%; Score 1416; DB 5; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.9e-87;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVRRPGSLRLSCAAGFTFDDYGMWVR 60
DB 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVRRPGSLRLSCAAGFTFDDYGMWVR 60
QY 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAR 120
QY 121 MRAPVIMGGQTLTVTSRGGSGGGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180
DB 121 LTHPYFMGGQTLTVTSRGGSGGGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180
QY 181 YVASWYQOKRPGQAPVLYVIGKNNRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240
DB 181 YVASWYQOKRPGQAPVLYVIGKNNRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240
QY 241 RDSSGNHVVFGGCTKLTIVGAAAEOKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGCTKLTIVGAAAEOKLISEEDLNGAA 277

```

RESULT 5
ABG92019
ID ABG92019 standard; protein; 277 AA.
XX
XX
AC ABG92019;
XX
DT 04-DEC-2002 (first entry)
XX
XX Human antibody fragment #203.
DE
XX
XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX metastasis; hypervariable region; autoimmune disease; thrombosis;
XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX myocardial infarction; retinopathic disease; abnormal platelet function;
XX sulphated tyrosine-dependent protein-protein interaction.
XX
XX Homo sapiens.
OS
XX
XX WO200253700-A2.
XX
XX 11-JUL-2002.
XX
XX 31-DEC-2001; 2001WO-US049442.
XX
XX 29-DEC-2000; 2000US-00751181.
XX
XX 29-DEC-2000; 2000US-0258948P.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX Stanthon E, Richter T, Amit B, Kooperman L, Perez T, Levanon A;
XX WPI; 2002-674776/72.
XX
XX Novel isolated epitope present on cancer cells and important in
XX physiological phenomena such as cell rolling, metastasis and
XX inflammation, for treating autoimmune, inflammatory or cardiovascular
XX diseases, and cancer.
XX
XX Claim 23; Page 308-309; Opp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
XX important in physiological phenomena such as cell rolling, metastasis and
XX inflammation, where the epitope is capable of being bound by an antibody,
XX its antigen-binding fragment or its complex comprising at least one
XX antibody or its binding fragment having a first hypervariable region. The
XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
XX disease, thrombosis, restenosis, metastasis, growth and/or replication of
XX tumour or leukaemia cells, increase in number of tumour or leukaemia
XX cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
XX platelet and/or cell-platelet adhesion or aggregation, for increasing
XX mortality of tumour or leukaemia cells, for increasing the susceptibility
XX of diseased cells to damage by anti-disease, anti-cancer or anti-
XX leukemia agents, or for decreasing the number of tumour or leukaemia
XX cells in a patient, or in the manufacture of a medicament for the above
XX mentioned purposes. The epitopes are useful for diagnosing and treating
XX diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
XX diseases, cardiovascular diseases such as myocardial infarction,
XX retinopathic diseases and other diseases mediated by abnormal platelet
XX function and diseases caused by sulphated tyrosine-dependent protein-
XX protein interactions. This sequence represents a human antibody fragment
XX of the invention
XX
XX Sequence 277 AA;
XX
XX Query Match 98.3%; Score 1416; DB 5; Length 277;
XX Best Local Similarity 98.2%; Pred. No. 1.9e-87;
XX Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 MKTILPTAAGLLLLAQAQMAAEVQLVESGGGVVPRPGSRLSCAASGFTFDYGMWVR 60
XX 1 MKTILPTAAGLLLLAQAQMAAEVQLVESGGGVVPRPGSRLSCAASGFTFDYGMWVR 60

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XX
XX 61 QAPKGLKLVNVSGLNNNGSGTGYADSVKGRFTISRDNKNSLYIQNNSLRAEDPAVYYCAR 120
XX 61 QAPKGLKLVNVSGLNNNGSGTGYADSVKGRFTISRDNKNSLYIQNNSLRAEDPAVYYCAR 120
XX
XX 121 MRAPVIMGGGTLVTVVRGGGSGGGSGGSSSELTPDPVAVSVALGQTVRITCGDSLS 180
XX 121 LTHPYFGGCTLVTVVRGGGSGGGSGGSSSELTPDPVAVSVALGQTVRITCGDSLS 180
XX
XX 181 YVASWYQQRGQAPVLVIYVKNNRPSGIPDRFSGSSSGNTASITTTGAQDEADYYCNS 240
XX 181 YVASWYQQRGQAPVLVIYVKNNRPSGIPDRFSGSSSGNTASITTTGAQDEADYYCNS 240
XX
XX 241 RDSGGNHVYFGGCTKLTIVGAARLISEEDLNGAA 277
XX 241 RDSGGNHVYFGGCTKLTIVGAARLISEEDLNGAA 277
XX
XX RESULT 6
XX ADI28367
XX ID ADI28367 standard; protein; 278 AA.
XX
XX ADI28367;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human scFv fragment Y17, binds to platelets.
XX
XX Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX
XX Homo sapiens.
XX
XX WO2004002528-A1.
XX
XX 08-JAN-2004.
XX
XX 30-JUN-2003; 2003WO-US020604.
XX
XX 01-JUL-2002; 2002US-00189025.
XX
XX (SAVI-) SAVIENT PHARM INC.
XX
XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX WPI; 2004-099189/10.
XX
XX Composition comprising an agent and/or antibody or its fragment, useful
XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or
XX for inhibiting growth and/or replication of tumor cells or leukemia
XX cells.
XX
XX Claim 13; SEQ ID NO 2; 58pp; English.
XX
XX The present sequence is the protein sequence of human scFv fragment Y17.
XX This antibody was identified by screening a human antibody phage library
XX that has diversity only in the heavy chain CDR3 regions. Fixed human
XX platelets were screened in order to identify antibodies that bind
XX platelets. Y17 binds leukaemic cells. The invention relates to
XX compositions utilising an agent and an antibody or its fragment. The
XX agent is a toxin, radioisotope or pharmaceutical agent such as
XX dexamethasone. It is complexed or combined with or conjugated to the
XX antibody or its fragment. The agent and/or antibody can be present in the
XX composition as a sub-clinical amount, i.e. less than the amount generally
XX found to be clinically effective when the agent is administered alone.
XX The composition is used in claimed methods of: inhibiting cell rolling,
XX inflammation, thrombosis, restenosis, metastasis, the growth and/or
XX replication of tumour cells or leukaemia cells, an increase in number of
XX tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
XX platelet-platelet and/or cell-platelet complex formation, aggregation or
XX adhesion; increasing the mortality rate of tumour or leukaemia cells, the
XX susceptibility of disease cells to damage by anti-disease agents, and the
XX susceptibility of tumour or leukaemia cells to damage by anti-cancer
XX agents; and ameliorating the effects of a disease, preventing a disease,
XX treating a disease or inhibiting the progress of a disease.

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XX	Sequence 278 AA;	97.0%; Score 1397.5; DB 8; Length 278;	Best Local Similarity 97.8%; Pred. No. 3.3e-86;	Matches 272; Conservative 1; Mismatches 4; Indels 1; Gaps 1
QY	1 MKYLLPTAAAGLLLLAQPAMAEVQVVEGCGVVRPGSLRLSCAASGTFPD-DYGMSTV	59		
DB	1 MKYLLPTAAAGLLLLAQPAMAEVQVVEGCGVVRPGSLRLSCAASGTFPDTHPYFVW	60		
QY	60 ROAPKGLGVWVGINWNGSGTGADSVKSRFTISRMAKNSLYLQNNSLRAEDTAYYYCA	119		
DB	61 ROAPKGLGVWVGINWNGSGTGADSVKSRFTISRMAKNSLYLQNNSLRAEDTAYYYCA	120		
QY	120 RMRAPVINGQGTLLVTVSRGGSGSGGGSGSGGSSBELTODPAVSVALGQTVRITCGDSL	179		
DB	121 RMRAPVINGQGTLLVTVSRGGSGSGGGSGSGGSSBELTODPAVSVALGQTVRITCGDSL	180		
QY	180 SYTAAWYQOKPCQAPVLYLYGKNNRPSGIPDRFSGSSSGNTYASLTITGAQAEADYYCN	239		
DB	181 SYTAAWYQOKPCQAPVLYLYGKNNRPSGIPDRFSGSSSGNTYASLTITGAQAEADYYCN	240		
QY	240 SRDSSGNHVFGGSGTKLTVLGAABEOKLISEEDLNGAA	277		
DB	241 SRDSSGNHVFGGSGTKLTVLGAABEOKLISEEDLNGAA	278		
RESULT 7				
ADJ57363				
ID	ADJ57363 standard; protein; 280 AA.			
XX	ADJ57363;			
AC	ADJ57363;			
XX				
DT	06-MAY-2004 (first entry)			
DE	P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32.			
XX				
KW	P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytosolic;			
KV	antiflammatory; immunosuppressive; human.			
OS	Homo sapiens.			
XX				
XX	Key	Location/Qualifiers		
FH	Region	53..60		
FT		/label= CDR1		
FT		/note= "Specifically referred to in Claim 2"		
FT	Region	75..90		
FT		/label= CDR2		
FT		/note= "Specifically referred to in Claim 2"		
FT	Region	124..129		
FT		/label= CDR3		
FT		/note= "Specifically referred to in Claim 2"		
XX				
XX	WO2004003166-A2.			
XX				
XX	08-JAN-2004.			
XX				
XX	30-JUN-2003; 2003WO-US020602.			
XX				
XX	01-JUL-2002; 2002US-00189032.			
XX				
XX	(SAVI-) SAVIENT PHARM INC.			
XX				
XX	Levanon A, Ben-Levy R, Plakstin D, Szanton E, Hagat Y;			
XX	Hoch Mer- Chaim H;			
XX				
XX	WPI; 2004-203378/19.			
XX				
XX	Novel antibody or its fragment that binds to an epitope of P-Selectin-			
XX	Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,			
XX	infection, auto-immune disease, metastasis, tumor/leukemia cell in			
XX	patient.			

XX	Claim 1; SEQ ID NO 1; 106pp; English.	
CC	The present sequence is that of an scFv antibody fragment, designated	
CC	L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody	
CC	was identified by screening a phage library, which had diversity only in	
CC	the heavy chain CDR3 regions, against a leukaemia cell to select specific	
CC	antibodies that recognised leukaemia cell surface determinants, wherein	
CC	the specific receptor was not previously known or characterised. The	
CC	invention relates to an antibody or its fragment having the binding	
CC	capabilities of L32. Such antibodies can be used in therapeutic,	
CC	diagnostic, prognostic and staging methods. Pharmaceutical compositions	
CC	comprising such antibodies are used to treat conditions related to:	
CC	inhibiting or treating cell rolling, inflammation, autoimmune disease,	
CC	infection (e.g. HIV infection), metastasis, and growth and/or replication	
CC	of tumour cells; increasing the mortality of tumour cells; inhibiting	
CC	growth and/or replication of tumour cells; inhibiting growth and/or	
CC	replication of leukaemia cells; increasing the mortality rate of	
CC	leukaemia cells; altering the susceptibility of diseased cells to damage	
CC	by anti-disease agents; increasing the susceptibility of tumour cells to	
CC	damage by anti-cancer agents; increasing the susceptibility of leukaemia	
CC	cells to damage by anti-leukaemia agents; inhibiting increase in number	
CC	of tumour cells in a patient; decreasing the number of tumour cells in a	
CC	patient; inhibiting increase in number of leukaemia cells in a patient;	
CC	and decreasing the number of leukaemic cells in a patient. Other methods	
CC	are provided to induce antibody-dependent cell-mediated cytotoxicity or	
CC	stimulate natural killer or T cells using the antibodies. A method of	
CC	pulsing tumour cells from a patient involves incubating the cells with	
CC	the antibody.	
XX		
XX	Sequence 280 AA:	
XX		
XX	Query Match	96.8%; Score 1393.5; DB 8; Length 280;
XX	Best Local Similarity	97.1%; Pred. No. 6.1e-86;
XX	Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1,	
QY	1 MKYLLPTRAAGLILIAAQPMAAEVQLVESGGGVVPRGSSLRLSCAASGFTD--DYGMS 57	
DB	1 MKYLLPTRAAGLILIAAQPMAAEVQLVESGGGVVPRGSSLRLSCAASGFTDLPKVKQM 60	
QY	58 WVRAPGKGLIEWVSGIMWNGGSTGYAIVSKGRFTISRDNKNSLYLQNNSLRAEPTAVYY 117	
DB	61 WVRAPGKGLIEWVSGIMWNGGSTGYAIVSKGRFTISRDNKNSLYLQNNSLRAEPTAVYY 120	
QY	118 CARRAPVINGQGLTVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITTCGDS 177	
DB	121 CARRAPVINGQGLTVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITTCGDS 180	
QY	178 LRSYASWYQQKPKQAPVLTVYIGNKRRPSGIPDRFSGSSSGNTASLTITGAQEDVDYY 237	
DB	181 LRSYASWYQQKPKQAPVLTVYIGNKRRPSGIPDRFSGSSSGNTASLTITGAQEDVDYY 240	
QY	238 CNSRDSGNNHYVPGSGTKLTVTGAAAROKLISEDLNGAA 277	
DB	241 CNSRDSGNNHYVPGSGTKLTVLGAAAROKLISEDLNGAA 280	
XX		
XX	RESULT 8	
XX	AD128368	
XX	ID AD128368 standard; protein; 280 AA.	
XX	XX AD128368;	
XX	AC	
XX	DT 06-MAY-2004 (first entry)	
XX	DE Human scFv fragment L32, binds to leukaemia cells.	
XX	KW Human; antibody; scFv; leukaemia; drug delivery; cancer; therapy.	
XX	OS Homo sapiens.	
XX	XX WO2004002528-A1.	
XX	XX	

PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020604.
 XX
 PR 01-JUL-2002; 2002US-00189025.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 XX WPI; 2004-099189/10.
 DR
 XX Composition comprising an agent and/or antibody or its fragment, useful
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 PT for inhibiting growth and/or replication of tumor cells or leukemia
 PT cells.
 XX
 PS Claim 13; SEQ ID NO 3; 58pp; English.
 XX
 CC The present sequence is the protein sequence of human scFv fragment L32.
 CC This antibody was identified by screening a human antibody phage library
 CC that has diversity only in the heavy chain CDR3 regions. Leukemia cells
 CC were screened to select specific antibodies that recognise leukemia cell
 CC surface determinants. The invention relates to compositions utilising an
 CC agent and an antibody or its fragment. The agent is a toxin, radioisotope
 CC or pharmaceutical agent such as doxorubicin. It is complexed or combined
 CC with or conjugated to the antibody or its fragment. The agent and/or
 CC antibody can be present in the composition is a sub-clinical amount, i.e.
 CC less than the amount generally found to be clinically effective when the
 CC agent is administered alone. The composition is used in claimed methods
 CC of: inhibiting cell rolling, inflammation, thrombosis, restenosis,
 CC metastasis, the growth and/or replication of tumor cells or leukemia
 CC cells, an increase in number of tumor or leukemia cells, cell-cell,
 CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet
 CC complex formation, aggregation or adhesion; increasing the mortality rate
 CC of tumor or leukemia cells, the susceptibility of disease cells to
 CC damage by anti-disease agents, and the susceptibility of tumor or
 CC leukemia cells to damage by anti-cancer agents; and ameliorating the
 CC effects of a disease, preventing a disease, treating a disease or
 CC inhibiting the progress of a disease.
 CC
 XX Sequence 280 AA;
 SQ
 Query Match 96.3%; Score 1386.5; DB 8; Length 280;
 Best Local Similarity 96.8%; Pred. No. 1.8e-85;
 Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 QY 1 MKTLLPTAAAGLLILAAQPMMAEVLVESGGGVTRPGSGIRLSCAASGFTFDYGM 57
 DB 1 MKTLLPTAAAGLLILAAQPMMAEVLVESGGGVTRPGSGIRLSCAASGFTFDYGM 60
 QY 58 WVAQAPKGLIEWYSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADPTAVY 117
 DB 61 WVAQAPKGLIEWYSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADPTAVY 120
 QY 118 CARMRAPIVINGGGLTVIVSRGGSGGSGGSSSLTQDPVAVVALGQTVIRITCGDS 177
 DB 121 CARMRAPIVINGGGLTVIVSRGGSGGSGGSSSLTQDPVAVVALGQTVIRITCGDS 180
 QY 178 LRSYVASWYOQKPGQAPVLVIYGNKNNRPSGIPDRFSSSSSGNTASLTITTAQADEADYY 237
 DB 181 LRSYVASWYOQKPGQAPVLVIYGNKNNRPSGIPDRFSSSSSGNTASLTITTAQADEADYY 240
 QY 238 CNSRDSGNNHVVFGGGLTKLTVLGAQAEOKLISEEDINGAA 277
 DB 241 CNSRDSGNNHVVFGGGLTKLTVLGAQAEOKLISEEDINGAA 280

XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #204.
 XX
 KW Human; antibody; epitope; cancer; tumor; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 DR
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Page 309-310; 0pp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumor or leukemia cells, increase in number of tumor or leukemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumor or leukemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukemia agents, or for decreasing the number of tumor or leukemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 CC
 XX Sequence 266 AA;
 SQ
 Query Match 95.7%; Score 1378; DB 5; Length 266;
 Best Local Similarity 99.2%; Pred. No. 6.4e-85;
 Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKTLLPTAAAGLLILAAQPMMAEVLVESGGGVTRPGSGIRLSCAASGFTFDYGM 60
 DB 1 MKTLLPTAAAGLLILAAQPMMAEVLVESGGGVTRPGSGIRLSCAASGFTFDYGM 60
 QY 61 QAPKGLIEWYSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADPTAVYCAR 120
 DB 61 QAPKGLIEWYSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADPTAVYCAR 120
 QY 121 MRAPVIWGGLTVIVSRGGSGGSGGSSSLTQDPVAVVALGQTVIRITCGDSLRS 180

RESULT 9
 ABG92020
 ID ABG92020 standard; protein; 266 AA.
 XX
 AC ABG92020;

Db 121 MRAPVINGQGGTLVTVSRGGGSGGGGSSSELTODPAVSVALGQTVRITCGDSLRS 180
 QY 181 YVASWYQKPGQAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
 Db 181 YVASWYQKPGQAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
 QY 241 RDSGNNHVFEGGCTKLTVLGAABEQK 266
 Db 241 RDSGNNHVFEGGCTKLTVLGAABAKAK 266

RESULT 10

ADN06989 ID ADN06989 standard; protein; 291 AA.

AC ADN06989;

DT 01-JUL-2004 (first entry)

DE Human EGFR bs-scFv antibody protein, HER3.B12.

KW Bispecific single chain; bs-scFv; cancer;

KM epidermal growth factor receptor; EGFR; therapy; antibody; human.

OS Homo sapiens.

PN US2004071696-A1.

PD 15-APR-2004.

PF 04-APR-2003; 2003US-00406830.

PR 05-APR-2002; 2002US-0370276P.

PA (REGC) UNIV CALIFORNIA.

PA (FOX-C) FOX CHASE CANCER CENT.

PI Adams GP, Horak EM, Weiner LM, Marks JD;

DR WPI; 2004-328525/30.

PT Novel bispecific antibody comprising first and second antibody joined to each other and having binding specificity to different epitopes of Epidermal Growth Factor Receptor protein, useful for treating cancer.

PS Claim 14; SEQ ID NO 6; 57bp; English.

CC The present invention provides bispecific single chain (bs-scFv) antibody molecules which may be used to treat various forms of cancer associated with the overexpression of the epidermal growth factor receptor (EGFR) family. The invention is useful for specifically delivering an effector molecule to a cell bearing a receptor from EGFR protein family chosen from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the treatment of cancer. The present sequence is human EGFR bs-scFv antibody protein.

CC Sequence 291 AA;

Query Match 89.9%; Score 1294; DB 8; Length 291;
 Best Local Similarity 88.8%; Pred. No. 3.2e-79;
 Matches 253; Conservative 10; Mismatches 14; Indels 8; Gaps 2;

QY 1 MKTLLPRAAAGLLILAAQPMABEVLVSGGGVTRPGGSLRLSCAASGTFDDYGMKSWR 60
 Db 1 MKTLLPRAAAGLLILAAQPMABEVLVSGGGVTRPGGSLRLSCAASGTFDDYGMKSWR 60
 QY 61 QAPGKGLWYSGINWNGSGTVGADSVKGRFTISRDNAKNSLYIQMNSLRAPEDYAVYYCAR 120
 Db 61 QAPGKGLWYSGINWNGSGTVGADSVKGRFTISRDNAKNSLYIQMNSLRAPEDYAVYYCAR 120
 QY 121 MRAPVINGQGGTLVTVSRGGGSGGGGSSSELTODPAVSVALGQTVRIT 172
 Db 121 MRAPVINGQGGTLVTVSRGGGSGGGGSSSELTODPAVSVALGQTVRIT 172

Db 121 DLGAKQWLEBFDYWGQGLTVTVSRGGGSGGGGSSFMFLTODPAVSVALGQTVRIT 180
 QY 173 CGDPSLRSYAASWYQKPGQAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAE 232
 Db 181 CGDPSLRSYAASWYQKPGQAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAE 240
 QY 233 EADYYCNSRDSGNNHVFEGGCTKLTVLGAABEQKLTISEEDLNGAA 277
 Db 241 EADYYCNSRDSGNNHVFEGGCTKLTVLGAABEQKLTISEEDLNGAA 285

RESULT 11

AAE02185 ID AAE02185 standard; protein; 282 AA.

AC AAE02185;

DT 10-AUG-2001 (first entry)

DE PAM1 single chain variable region (scFv) antibody.

KW Pectin; PAM1 antibody; single chain variable region; scFv; food; jam;

KM yogurt; gel; homogalacturonan; HG; plant cell wall.

OS Unidentified.

PH Key Location/Qualifiers

FT Peptide 1..22 /label=pe1B_leader_sequence

FT Region 23..140 /label=Heavy_chain_fragment

FT Region 141..156 /label=linker

FT Region 157..277 /label=light_chain_fragment

FT Region 267..277 /label=Myc_epitope

FT Misc-difference 277..282 /note="Encoded by AAT"

XX US6228599-B1.

XX 08-MAY-2001.

XX 26-FEB-1999; 99US-00260527.

XX 24-DEC-1998; 98GB-00028700.

XX (DANI-) DANISCO AS.

XX PI Knox JP, Willats WGT, Mikkelsen JD;

XX WPI; 2001-342672/36.

XX DR N-PSDB; AAD06193.

PT New PAM1 and PAM2 antibodies capable of binding de-esterified homogalacturonan, useful for identifying a pectin moiety, for quantifying the amount of pectin in a sample or for extracting pectin from a sample.

PS Claim 1; Fig 4B; 21bp; English.

CC The invention relates to antibodies specific to pectin, such as PAM1 and PAM2 scFv (single chain variable region). These antibodies are derived from a naive phage display library known as the synthetic scFv Library (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified CC and un-substituted homogalacturonan (HG), useful for identifying a pectin CC motif. PAM antibody is useful for identifying a pectin functional group CC and in assays to determine if a particular pectin composition has the CC pectin motif or can be used to prepare a food for human and animal CC consumption, such as jams, yogurts or gels. The PAM antibodies are CC further useful for quantifying the amount of pectin in a sample or for CC extracting pectin from a sample. PAM antibodies are also used to identify CC de-esterified homogalacturonan blocks in the primary cell walls of

CC plants. The present sequence is PAM1 scfv antibody specific to pectin.
 CC Note: This sequence is stated as being the same as that shown as SEQ ID
 CC NO: 1 in the sequence listing of the specification, however the sequence
 CC has 2 extra residues at the C-terminal end

XX Sequence 282 AA;

Query Match 88.8%; Score 1278.5; DB 4; Length 282;
 Best Local Similarity 90.0%; Pred. No. 3,4e-78;
 Matches 252; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

QY 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVVRPGGSLRLSCAASGFTEDDYGMWVR 60
 DB 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVVRPGGSLRLSCAASGFTESNMMWVR 60
 QY 61 QAAGKGIEMWVSGI--MNAGSTGYADSVKGRFTISPDNAKNSLYLQNSLRADDTAVYVC 118
 DB 61 QAAGKGIEMWVSGI--MNAGSTGYADSVKGRFTISPDNAKNSLYLQNSLRADDTAVYVC 120
 QY 119 AR-MRAPVWVGQGLTVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITCOGDS 177
 DB 121 ARKMRKRLRWGGGLTVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITCOGDS 180
 QY 178 LRSYVASWYQKPGQAPFVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDADYY 237
 DB 181 LRSYVASWYQKPGQAPFVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDADYY 240
 QY 238 CNSRDSGGNHVVFSGGKTLVLGAAPAEOKLISEEDLNGAA 277
 DB 241 CNSRDSGGNHVVFSGGKTLVLGAAPAEOKLISEEDLNGAA 280

RESULT 12

AAW83322 standard; protein; 309 AA.
 ID AAW83322;

AC AAW83322;

DT 16-MAR-1999 (first entry)

XX Single chain Apo-2 antibody 16E2.

XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
 KM tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
 KM TNF cytokine.

OS Homo sapiens.

XX WC9851793-A1.

XX 19-NOV-1998.

PD 14-MAY-1998; 98WC-US009704.

XX 15-MAY-1997; 97US-00857216.

PR 09-FEB-1998; 98US-00020746.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Adams CW, Chuntharapai A, Kim KJ;

DR WPI, 1999-045228/04.

DR N-PSDB; AAV72532.

XX Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions
 PT linked with decreased apoptosis e.g. cancer, and produce antibodies to
 PT increase or decrease apoptosis.

XX Example 14; Fig 16; 134pp; English.

CC The present invention describes human Apo-2. Apo-2 can be used
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful
 CC to treat conditions associated with decreased apoptosis e.g. cancer. Apo-

CC 2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR).
 CC TNF cytokines can induce apoptosis, thought to be initiated by binding to
 CC TNFR, and Apo-2 triggered caspase-dependent apoptosis. It can be used to
 CC identify agents activating Apo-2, useful to treat mammalian cancer cells,
 CC and to produce Apo-2 chimeras useful therapeutically (e.g. those
 CC containing immunoglobulin sequences can be inhibit apoptosis) or
 CC diagnostically (e.g. those comprising an epitope tag polypeptide allow
 CC Apo-2 detection and purification using anti-tag antibodies). It can be
 CC used to produce antibodies which can be combined with a (particularly
 CC pharmaceutically acceptable) carrier in compositions or used to produce
 CC dimeric molecules (especially homodimeric molecules comprising first and
 CC second Apo-2 antibodies). Agonistic (especially single-chain) antibodies
 CC can be administered to induce apoptosis in mammalian cancer cells, and
 CC antagonistic antibodies used to block excessive apoptosis (e.g. in
 CC neurodegenerative diseases). Apo-2 antibodies may also be used
 CC diagnostically e.g. to detect Apo-2 expression in cells/tissues and in
 CC Apo-2 purification. The present sequence represents a single chain Apo-2
 CC antibody, designated 16E2

XX Sequence 309 AA;

Query Match 88.6%; Score 1275.5; DB 2; Length 309;
 Best Local Similarity 89.9%; Pred. No. 5,9e-78;
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

QY 16 AQPMAAEVOLVESGGGVVRPGGSLRLSCAASGFTEDDYGMWVRQAPGKLEWVSGINW 75
 DB 33 AQPMAAEVOLVSGGGGVVRPGGSLRLSCAASGFTEDDYGMWVRQAPGKLEWVSGINW 92
 QY 76 NGSTGYADSVKGRFTISPDNAKNSLYLQNSLRADDTAVYCARAP-----VINGQ 129
 DB 93 NGSTGYADSVKGRFTISPDNAKNSLYLQNSLRADDTAVYCARAP-----VINGQ 152
 QY 130 GTLVTVSRGGSGSGGSGGSSSELTQDPAVSVALGQTVRITCOGDSLRSYASWYQOK 189
 DB 153 GTLVTVSRGGSGSGGSGGSSSELTQDPAVSVALGQTVRITCOGDSLRSYASWYQOK 212
 QY 190 PGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNSRDSGGNHV 249
 DB 213 PGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNSRDSGGNHV 272
 QY 250 FGGGTKLTVLGA-----AAEQKLISEEDLNGAA 277
 DB 273 FGGGTKLTVLGAHHHHRGAAPAEOKLISEEDLNGAA 309

RESULT 13

ABB09603 standard; protein; 309 AA.
 ID ABB09603

XX ABB09603;

DT 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 16E2.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis; caspase;
 KM apoptosis; cancer; antibody.

XX Bacteriophage.

OS US6342369-B1.

PN 29-JAN-2002.

PD 14-MAY-1998; 98US-00079029.

XX 15-MAY-1997; 97US-0046615P.

PR 09-FEB-1998; 98US-0074119P.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ;

XX WPI; 2002-224941/28.
 DR N-PSDB; ABL41733.
 XX
 PT New nucleic acids encoding an Apo-2 ligand, useful for activating or
 PT stimulating apoptosis in cancer cells, thus especially useful in the
 PT treatment of cancer, or in enhancing immune-mediated cell death.
 XX
 PS Example 14; Fig 16; 68pp; English.
 XX
 CC The present sequence represents a single-chain Apo-2 antibody, designated
 CC 16B2, which is isolated from a phage library. It is believed that Apo-2
 CC is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2
 CC polypeptide is capable of triggering caspase-dependent apoptosis and
 CC activating nuclear factor-kappa B. A soluble extracellular domain of Apo-
 CC 2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate
 CC or stimulate apoptosis in cancer cells. They are therefore especially
 CC useful in the treatment of cancer, to enhance immune-mediated cell death
 CC in cells expressing Apo-2, to detect expression of Apo-2 in specific
 CC cells, tissues or serum, and in affinity purification of Apo-2 from
 CC recombinant cell culture or natural sources
 XX
 SQ Sequence 309 AA;
 Query Match 88.6%; Score 1275.5; DB 5; Length 309;
 Best Local Similarity 89.9%; Pred. No. 5.9e-78;
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;
 QY 16 AADPAAAEVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 75
 DB 33 AADPAAAEVOLVSGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 92
 QY 76 NGSGTAVSVKRFITSRDNANKNSLYLQWNSLRABDTAVYYCARMRAP-----VIWQ 129
 DB 93 NGSGTAVSVKRFITSRDNANKNSLYLQWNSLRABDTAVYYCARMRAP-----VIWQ 152
 QY 130 GTLVTVSRGGGSGGGGSGGSSSELTPDPAVSVALGQTVRITCQGDLSLSYASWYQOK 189
 DB 153 GTLVTVSRGGGSGGGGSGGSSSELTPDPAVSVALGQTVRITCQGDLSLSYASWYQOK 212
 QY 190 PGQAPLVLYGKNNRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 249
 DB 213 PGQAPLVLYGKNNRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 272
 QY 250 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 277
 DB 273 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 309

RESULT 14
 ABL41733
 ID ABL41733 standard; protein; 309 AA.
 AC ABL41733;
 XX
 DT 11-APR-2003 (first entry)
 XX
 DE Single chain antibody (scFv) fragment 16B2.
 XX
 KW Apo-2; tumour necrosis factor family; TNFR; gene therapy; apoptosis;
 KW tissue-specific typing; affinity purification;
 KW competitive-type receptor binding assay; mouse; 16B2.
 XX
 OS Mus sp.
 XX
 PN US2002150985-A1..
 XX
 PD 17-OCT-2002.
 XX
 PF 02-NOV-2001; 2001US-00052798.
 XX
 PR 15-MAY-1997; 97US-0046615P.
 PR 09-FEB-1998; 98US-0074119P.

PR 14-MAY-1998; 98US-00079029.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Ashkenazi AJ, Chuntharapat A, Kim KJ;
 XX WPI; 2003-198287/19.
 DR N-PSDB; ABX16407.
 XX
 PT New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis
 PT in mammalian cells, in vivo or ex vivo gene therapy, in quantitative
 PT diagnostic assays, or in generating antibodies against Apo-2.
 XX
 PS Example 14; Fig 16; 64pp; English.
 XX
 CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control
 CC against samples containing unknown quantities of Apo-2, in generating
 CC antibodies, in affinity purification techniques, and in competitive-type
 CC receptor binding assays when labelled with, for instance, radioiodine,
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a
 CC diagnostic for tissue-specific typing. This is the amino acid sequence of
 CC the single chain antibody fragment (scFv) 16B2 used in the preparation of
 CC anti-apo-2 antibodies
 XX
 SQ Sequence 309 AA;
 Query Match 88.6%; Score 1275.5; DB 6; Length 309;
 Best Local Similarity 89.9%; Pred. No. 5.9e-78;
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;
 QY 16 AADPAAAEVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 75
 DB 33 AADPAAAEVOLVSGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 92
 QY 76 NGSGTAVSVKRFITSRDNANKNSLYLQWNSLRABDTAVYYCARMRAP-----VIWQ 129
 DB 93 NGSGTAVSVKRFITSRDNANKNSLYLQWNSLRABDTAVYYCARMRAP-----VIWQ 152
 QY 130 GTLVTVSRGGGSGGGGSGGSSSELTPDPAVSVALGQTVRITCQGDLSLSYASWYQOK 189
 DB 153 GTLVTVSRGGGSGGGGSGGSSSELTPDPAVSVALGQTVRITCQGDLSLSYASWYQOK 212
 QY 190 PGQAPLVLYGKNNRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 249
 DB 213 PGQAPLVLYGKNNRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 272
 QY 250 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 277
 DB 273 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 309

RESULT 15
 ADG98737
 ID ADG98737 standard; protein; 309 AA.
 AC ADG98737;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human single chain antibody (scFv) 16B2 protein.
 XX
 KW Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
 KW cancer; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PH Key
 FT Peptide
 FT Protein
 FT
 FT Location/Qualifiers
 1..12
 /label=Signal_peptide
 13..309
 /note="Human mature single chain antibody protein"

FT	Region	70..74	/note= "Heavy chain CDR1"
FT		/note= "Heavy chain complementarity determining region 1"	
FT	Region	89..105	/note= "Heavy chain CDR2"
FT		/note= "Heavy chain complementarity determining region 2"	
FT	Region	138..149	/note= "Heavy chain CDR3"
FT		/note= "Heavy chain complementarity determining region 3"	
FT	Region	197..206	/note= "Light chain CDR1"
FT		/note= "Light chain complementarity determining region 1"	
FT	Region	223..229	/note= "Light chain CDR2"
FT		/note= "Light chain complementarity determining region 2"	
FT	Region	262..272	/note= "Light chain CDR3"
FT		/note= "Light chain complementarity determining region 3"	
XX		US2003148455-A1.	
XX		07-AUG-2003.	
XX		06-NOV-2002; 2002US-00288917.	
XX		15-MAY-1997; 97US-0046615P.	
PR		09-FEB-1998; 98US-0074119P.	
PR		14-MAY-1998; 98US-00079029.	
PR		02-NOV-2001; 2001US-00052798.	
XX		(GETH) GENENTECH INC.	
XX			
PI	Adams CW, Aeshkenazi AJ, Chuntcharapai A, Kim KJ;		
XX		WPI: 2003-897574/82.	
DR	N-PsDB; ADG98734.		
XX			
PT	New Apo-2 polypeptide or its extracellular or death domain sequence,		
PT	useful for modulating apoptosis in mammalian cancer cells or for		
PT	generating transgenic or knockout animals.		
XX			
PS	Example 14; SEQ ID NO 9; 64pp; English.		
XX			
CC	The present invention provides novel Apo-2 protein and the nucleic acid		
CC	encoding the protein. The invention is useful in inducing apoptosis in		
CC	mammalian cancer cells. The invention is also useful in diagnostic		
CC	procedures for tissue-specific typing and in generating transgenic		
CC	animals that are useful in development and screening of reagents. The		
CC	invention is also useful in gene therapy. The present sequence is human		
CC	single chain antibody (scfv) protein.		
XX			
SQ	Sequence 309 AA:		
	Query Match	88.6%; Score 1275.5; DB 7; Length 309;	
	Best Local Similarity	89.9%; Pred. No. 5.9e-78;	
	Matches 249; Conservative	5; Mismatches 8; Indels 15; Gaps 2;	
OY	16 AAOPMAAEVLVESGGGVVRPGSGRLSCAASGFTPEDYIGMSWRQAQKGLIEWSGINW	75	
Db	33 AAOPMAAEQLVQSQGVRRPGSRLSCAASGFPPDYIGMSWRQAQKGLEWVGINW	92	
OY	76 NGSGTGYADSVYGRFTISRDNAKNSLYIQMMSLRADTVAVYYCAMRAP-----VIWGQ	129	
Db	93 NGSGTGYADSVYGRFTISRDNAKNSLYIQMMSLRADTVAVYYCAITLDAGRWYDLMGX	152	
OY	130 GTLVTVSRGGGSGGGGSSSELTDPAVSVALGQTTRITCGDSLRSYSASYWYQQ	189	
Db	153 GTTVTVSSGGGSGGGGSSSELTDPAPVSVALGQTVRITTCGDSLRSYSASYWYQQ	212	
OY	190 PGQAIVLVIYGNKNPSCIPIDFSSSSSGNTASTLTITAQADEADYYCNSDDSGNNVV	249	
Db	213 PGQAIVLVIYGNKNPSCIPIDFSSSSSGNTASTLTITAQADEADYYCNSDDSGNNVV	272	

```
Qy      250 FGGGKTLTVLGA-----AAEQKLISEEDLNGAA 277
          |||||
Db      273 FGGGTSLTVLGAALHHHGHGAAEQLIASEEDLNGAA 309
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OM protein - protein search, using sw model

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Title: US-10-029-926D-25

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A COMB pep:*
2: /cgn2_6/prodata/1/aa/5B COMB pep:*
3: /cgn2_6/prodata/1/aa/6A COMB pep:*
4: /cgn2_6/prodata/1/aa/6B COMB pep:*
5: /cgn2_6/prodata/1/aa/6C COMB pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1278.5	88.8	280	US-09-260-527-1	Sequence 1, Appl
2	1275.5	88.6	309	US-09-079-029-9	Sequence 9, Appl
3	1194	82.9	312	US-09-079-029-10	Sequence 10, Appl
4	1126.5	78.2	278	US-09-260-527-3	Sequence 3, Appl
5	973	67.6	310	US-09-079-029-11	Sequence 11, Appl
6	836.5	58.1	284	US-08-564-164A-2	Sequence 2, Appl
7	829	57.6	282	US-08-860-174A-10	Sequence 10, Appl
8	822	57.1	268	US-09-976-118-1	Sequence 1, Appl
9	803	55.8	240	US-09-192-854-2	Sequence 2, Appl
10	800	55.6	289	US-09-184-658-63	Sequence 63, Appl
11	800	55.6	289	US-09-504-262D-63	Sequence 63, Appl
12	797.5	55.4	334	US-09-646-028-53	Sequence 53, Appl
13	797.5	55.4	334	US-09-646-028-55	Sequence 55, Appl
14	791.5	55.0	348	US-09-646-028-51	Sequence 51, Appl
15	787.5	54.7	245	US-08-918-148-75	Sequence 75, Appl
16	787.5	54.7	245	US-08-918-148-73	Sequence 73, Appl
17	786.5	54.6	245	US-08-918-148-76	Sequence 76, Appl
18	786.5	54.6	245	US-09-138-091A-74	Sequence 74, Appl
19	786	54.6	255	US-09-553-498-8	Sequence 8, Appl
20	786	54.6	255	US-09-618-869-8	Sequence 8, Appl
21	781.5	54.3	245	US-08-918-148-78	Sequence 78, Appl
22	781.5	54.3	245	US-09-138-091A-76	Sequence 76, Appl
23	775	53.8	272	US-09-126-219A-163	Sequence 163, Appl
24	772.5	53.6	301	US-08-661-052-14	Sequence 14, Appl
25	772.5	53.6	301	US-09-188-082-14	Sequence 14, Appl
26	772.5	53.6	301	US-09-364-088-14	Sequence 14, Appl
27	772.5	53.6	301	US-09-102-716-14	Sequence 14, Appl

28	761	52.8	281	3	US-09-025-769B-178	Sequence 178, App
29	761	52.8	281	4	US-09-490-070A-178	Sequence 178, App
30	761	52.8	281	4	US-09-490-153-178	Sequence 178, App
31	761	52.8	281	4	US-09-490-324-178	Sequence 178, App
32	758	52.6	288	3	US-09-423-439-38	Sequence 38, Appl
33	757	52.6	244	3	US-08-918-148-77	Sequence 77, Appl
34	757	52.6	244	4	US-09-138-091A-75	Sequence 75, Appl
35	745.5	51.8	267	3	US-09-485-737B-2	Sequence 2, Appl
36	745.5	51.8	267	4	US-10-071-988-9	Sequence 9, Appl
37	744.5	51.7	402	2	US-08-491-988-9	Sequence 9, Appl
38	742.5	51.6	281	3	US-09-423-439-44	Sequence 44, Appl
39	739.5	51.4	415	2	US-08-491-988-7	Sequence 7, Appl
40	739.5	51.4	435	2	US-08-491-988-5	Sequence 5, Appl
41	737.5	51.2	269	2	US-08-428-257A-72	Sequence 72, Appl
42	737.5	51.2	269	2	US-08-491-988-3	Sequence 3, Appl
43	737	51.2	359	4	US-09-646-028-16	Sequence 16, Appl
44	731	50.8	265	2	US-08-403-853-16	Sequence 16, Appl
45	731	50.8	361	4	US-09-646-028-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYO019, 001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phase display library known as the Synthetic scFv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match 88.8%; Score 1278.5; DB 3; Length 280;
Best Local Similarity 90.0%; Pred. No. 1.9e-95;
Matches 252; Conservative 10; Mismatches 15; Indels 3; Gaps 2;
QY 1 MKYLLPTAAAGLLLAQAQA.....VLGAARQLISEEDLNGAA 277
DB 1 MKYLLPTAAAGLLLAQAQA.....VLGAARQLISEEDLNGAA 277
QY 61 QAPGKLELVSGI--NMNGSTGYADSVYGRFTISDANNSLYLQNSLRADTVAYYC 118
DB 61 QAPGKLELVSGI--NMNGSTGYADSVYGRFTISDANNSLYLQNSLRADTVAYYC 120
QY 119 AR-MRAPVIMGGTTLTVTSRGGSGGGSGGSSSELTPDPVSVALGQTVAITCGDS 177
DB 121 ARMRPALMGGTTLTVTSRGGSGGGSGGSSSELTPDPVSVALGQTVAITCGDS 180
QY 178 LRSYASWTQOKRGQAPVIVYIKNNRPSGIDPRFGSSSGNTASLTITGAQAEADY 237
DB 181 LRSYASWTQOKRGQAPVIVYIKNNRPSGIDPRFGSSSGNTASLTITGAQAEADY 240
QY 238 CNSRDSGHHVVFGGGKTITVGAARQLISEEDLNGAA 277
DB 241 CNSRDSGHHVVFGGGKTITVGAARQLISEEDLNGAA 280

```
RESULT 2
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9

Query Match      88.6%; Score 1275.5; DB 3; Length 309;
Best Local Similarity 89.9%; Pred. No. 3,7e-95;
Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

QY 16 AAQPAAAEVOLVSGGSGGVVPPGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINW 75
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 33 AAQPAAAEVOLVSGGSGGVVPPGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINW 92
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 76 NGSGTYADSVKGRFTISRDNKNSLYLQNMSLRADTAAYVYCARMPAP-----VTWGQ 129
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 93 NGSGTYADSVKGRFTISRDNKNSLYLQNMSLRADTAAYVYCARMPAP-----VTWGQ 152
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 130 GTLVTVSRGGSGGSGGSSSELTQDPAVSVVALGQTVRITCGDLSLSYYASWYQOK 189
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 153 GTLVTVSRGGSGGSGGSSSELTQDPAVSVVALGQTVRITCGDLSLSYYASWYQOK 212
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 190 PGQAPVLYVYIGKNNRPBGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNRSRDSGNHV 249
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 213 PGQAPVLYVYIGKNNRPBGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNRSRDSGNHV 272
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 250 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 277
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 273 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 309
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
```

```
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-10

Query Match      82.9%; Score 1194; DB 3; Length 312;
Best Local Similarity 85.0%; Pred. No. 1,4e-88;
Matches 238; Conservative 5; Mismatches 19; Indels 18; Gaps 2;

QY 16 AAQPAAAEVOLVSGGSGGVVPPGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINW 75
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 33 AAQPAAAEVOLVSGGSGGVVPPGSLRLSCAASGFTSSYVMSVROAPGKLEWVSGINW 92
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 76 NGSGTYADSVKGRFTISRDNKNSLYLQNMSLRADTAAYVYCARMPAP-----I 126
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 93 DGEKTYVDSVKGRFTISRDNKNSLYLQNMSLRADTAAYVYCARMDLKVKGSSSGMFPD 152
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 WGGTILTVSRGGSGGSGGSSSELTQDPAVSVVALGQTVRITCGDLSLSYYASWY 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 153 WGGTILTVSRGGSGGSGGSSSELTQDPAVSVVALGQTVRITCGDLSLSYYASWY 212
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 187 QOKPGAPVLYVYIGKNNRPBGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNRSRDSGN 246
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 213 QOKPGAPVLYVYIGKNNRPBGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNRSRDSGN 272
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 247 HVFVGGGTLTVLGA-----AAEQKLISEEDLNGAA 277
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 273 HVFVGGGTLTVLGA-----AAEQKLISEEDLNGAA 312
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willate, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9,001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
```

SEQ ID NO 3
LENGTH: 278
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
OTHER INFORMATION: from a naive phage display library known as the
OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match 78.2%; Score 1126.5; DB 3; Length 278;
Best Local Similarity 80.3%; Pred. No. 3.3e-83;
Matches 224; Conservative 17; Mismatches 35; Indels 3; Gaps 3;

QY 1 MKTLPAAAGLLILAAQPMABEVQVLSGGGCVTRPGSLRLSCAAGFTPDYDGM-SWV 59
DB 1 MKTLPAAAGLLILAAQPMABEVQVLSGGGCVTRPGSLRLSCAAGFTPDYDGM-SWV 60
QY 60 ROAPGKLEWVSGINMGSTGVADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCA 119
DB 61 RPPGKLEWV-GYIYSSGTYNPSLKSRYTMSVDTSKQFSLKSSVTRAVDIAVYYCA 119
QY 120 RMRAPVY-WGQGLTVYTRSGGSGGGSGGSGGSSSLTQDPAVSVALGQTVRTTCQDSL 178
DB 120 RMRAPVY-WGQGLTVYTRSGGSGGGSGGSGGSSSLTQDPAVSVALGQTVRTTCQDSL 179
QY 179 RSTYASWYQOKPGQAPVLYYGNRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYC 238
DB 180 RSTYASWYQOKPGQAPVLYYGNRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYC 239
QY 239 NSRDSGNNHVPFGGGLTVLTLGAABEOKLISEEDLNGAA 277
DB 240 NSRDSGNNHVPFGGGLTVLTLGAABEOKLISEEDLNGAA 278

RESULT 5

US-09-079-029-11
Sequence 11, Application US/09079029

PATENT No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11

Query Match 67.6%; Score 973; DB 3; Length 310;
Best Local Similarity 71.9%; Pred. No. 8.9e-71;
Matches 200; Conservative 19; Mismatches 43; Indels 16; Gaps 4;

QY 16 AAOPMABEVQVLSGGGCVTRPGSLRLSCAAGFTPDYDGM-SWVRAQPGKLEWVSGIN 75
DB 33 AAOPMABEVQVLSGGGCVTRPGSLRLSCAAGFTPDYDGM-SWVRAQPGKLEWVSGIN 92
QY 76 NGSTGVADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPV---IWGQGL 132
DB 93 DGNKTYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPV---IWGQGL 152
QY 133 VTVSSGGGSGGGSGGGSGGSSSLTQDPAVSVALGQTVRTTCQDSL---STYASWYQ 188
DB 153 VTVSSGGGSGGGSGGGSGGSSSLTQDPAVSVALGQTVRTTCQDSL---STYASWYQ 212
QY 189 KRGQAPVLYYGNRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGNNH 248
DB 213 LRGTAPEKLLYDSDNRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGNNH 272
QY 249 VFGGGLTVLTLGAABEOKLISEEDLNGAA 277
DB 273 VFGGGLTVLTLGAABEOKLISEEDLNGAA 310

RESULT 6

US-08-564-164A-2
Sequence 2, Application US/08564164A

PATENT No. 6153947
GENERAL INFORMATION:
APPLICANT: Schweighofer, Fabien
APPLICANT: Tocque, Bruno
TITLE OF INVENTION: Intracellular Binding Proteins and Use
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,164A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00714
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/07241
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST93030-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3816
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-564-164A-2

Query Match 58.1%; Score 836.5; DB 3; Length 284;
Best Local Similarity 62.2%; Pred. No. 8e-60;

Matches 171; Conservative 30; Mismatches 65; Indels 9; Gaps 4;

QY 7 TAAAGLLLLAQAAMAEVQLVESGGGVVPRGSLRLSCAASGFTPDYGMWVRQAPGK 66
DB 12 TAAAGLLLLAQAAMAEVQLVESGGGVVPRGSLRLSCAASGFTPDYGMWVRQAPGK 71
QY 67 LEVNSGINNNGSGTGVADSVKGRFTISRDNKNSLYIQNNSLRAEDTAVYICARMAP-- 124
DB 72 LEVNAVYSSGSSYLKYAEYVKGRFTISRDNKNTLYIQNTSLRSEDALYYCARHEGTGT 131
QY 125 ---VINGGGLTVNVRSGGSGSGGSGGSS--ELTQDP--AVGVALGQTVRITCQGDLSLR 179
DB 132 DFPDYWGQGTIVTVSSGGSGSGGSGGSDVELTQSPHSLNLSLGETVSIETLASGEGT 191
QY 180 SYVASWYQKPGQAPVLIYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCN 239
DB 192 SNYLAWYQKRGKSPQLIITYASSLDQGVSRFSGSGSGTQFSLKISNMQPEDBGVYYCQ 251
QY 240 SRDSSGNHVVFGGGLTVLGAAAEQKLISEEDLN 274
DB 252 QAYKYPG--TFGAGTKLEIKRAAAEQKLISEEDLN 284

RESULT 7

US-08-860-174A-10
Sequence 10, Application US/08860174A
Patent No. 5989830

GENERAL INFORMATION:

APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOOT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON, D.C.
STATE:
COUNTRY: UNITED STATES
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860.174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-860-174A-10

Query Match 57.6%; Score 829; DB 2; Length 282;
Best Local Similarity 61.7%; Pred. No. 3.2e-59;
Matches 177; Conservative 28; Mismatches 64; Indels 18; Gaps 7;

QY 1 MKYLPTAAAGLLLLAQAAMAEVQLVESGGGVVPRGSLRLSCAASGFTPDYGMWVR 60
DB 1 MKYLPTAAAGLLLLAQAAMAEVQLVESGGGVVPRGSLRLSCAASGFTPDYGMWVR 60
QY 61 QAPGKLEWVSGINNNGSGTGVADSVKGRFTISRDNKNSLYIQNNSLRAEDTAVYICAR 120
DB 61 QTSDEKLEWVATISSTDTYYTYSNDVNGRFTISRDNKNTLYIQNSLSLSEDTAVYICAR 120
QY 121 -----WRAPVIMQGTLYTVNVRSGGSGSGGSGGSS--ELTQDP--AVGVALGQTVRITC 173
DB 121 HGYYGKGYRDPYWGQGTIVTVSSGGSGSGGSGGSDLELTQSPHSLVTVTAGEXTVYMC 180
QY 174 Q-GDSL-----RSYVASWYQKPGQAPVLIYIGKNNRPSGIPDRFSGSSSGNTASLTITG 227
DB 181 KSGQSLINSVNQKNYLTWYQKPGQAPKLLIYVASTRESGVDPRTFASGSGTDFLTLLISS 240
QY 228 AQAEDEADYYCNSRDSGNNHVVFGGGLTVLGAAAEQKLISEEDLN 274
DB 241 VQAEDELAVYIC--QNDYTYPTFGGGLTKLEI--KREQKLISEEDLN 282

RESULT 8

US-09-976-118-1
Sequence 1, Application US/09976118
Patent No. 669473

GENERAL INFORMATION:

APPLICANT: Ratsch, Kevin Paul
APPLICANT: Curiel, David T.
APPLICANT: Bonner, James Allen
TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
TITLE OF INVENTION: Single-Chain Antibodies
FILE REFERENCE: D6355
CURRENT APPLICATION NUMBER: US/09/976.118
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,353
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 268
TYPE: PRT
ORGANISM: artificial sequence
FEATURES:
OTHER INFORMATION: amino acid sequence of anti-EGFR scfv
OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

Query Match 57.1%; Score 822; DB 4; Length 268;

Best Local Similarity 67.3%; Pred. No. 1.1e-58;
Matches 169; Conservative 21; Mismatches 47; Indels 14; Gaps 3;

QY 23 EVLVESGGGVVPRGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINNNGSGTGY 82
DB 1 EVLVESGGGVVPRGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINNNGSGTGY 60
QY 83 ADSVKGKFTISRDNKNSLYIQNNSLRAEDTAVYICARMAPV-----TWGGTLV 133
DB 61 ADSVKGKFTISRDNKNTLYIQNSLRAEDTAVYICVKDGGSSWYADYFDYWGQGTIV 120
QY 134 TVNRGGGGS-----CGGSGSGGSGSELTOPDAVVALGQTVRITCQGDLSLSYASWYQOK 169
DB 121 TVSSGSASAPKLEGESEARVQSVLTQPPSLVSFGQTASITCSGKLGDKTASWYQOK 180
QY 190 PGQAPVLIYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHV 249
DB 181 PGQSPVLIYQDKRPSGIPDRFSGSSSGNTATLITISGTQAMAEADYYCQAMKSSSTPY-V 239
QY 250 FGGGTLTVLG 260
DB 240 FGTGKTVTVLG 250

RESULT 9

US-09-192-854-2

```
Sequence 2, Application US/09192854
Patent No. 6696245
GENERAL INFORMATION:
APPLICANT: Winter, Greg
TITLE OF INVENTION: Methode for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
EARLIER FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-2

Query Match      55.8%; Score 803; DB 4; Length 240;
Best Local Similarity 66.2%; Pred. No. 3,3e-57;
Matches 153; Conservative 27; Mismatches 48; Indels 6; Gaps 4;

QY      23  EVQLVESGGGVVPRPGSLRLSCAASGFTPDYGMNWROAPGKGLEWVSGINMGSGTGY 82
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1  EVQLVESGGGVVPRPGSLRLSCAASGFTFSYAMSWROAPGKLEWVSAISGSGSTYY 60

DB
QY      83  ADSVKGRFTISRDNKASLYIQMNSLRADTAIVYCCARMAPV-ITGCGTLVTVSRGGCG 141
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61  ADSVKGRFTISRDNKASLYIQMNSLRADTAIVYCCARMAPVITGCGTLVTVSRGGCG 120

DB
QY      142  SGGGSGSGGSS--ELTQDP-AVSVALGQVTRITCGDLSRYYASMYQKPGQAPVLI 198
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      121  SGGGSGSGGSSITDIQMTPSSLSASVGDRTYITCRASGSISSLYLWYQKPGAPVLI 180

DB
QY      199  YGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCCNRDSSGNHVFSGGTLTV 258
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      181  YASLSLQSGVPSRSGSGGTDFLTLSIQPEDFAIYYCQGSYSTNP--TFGQGTIVEI 238

DB
RESULT 10
US-09-184-658-63
Sequence 63, Application US/09184658
Patent No. 6030792
GENERAL INFORMATION:
APPLICANT: Olteneasa, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downes, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: US/09/184,658
EARLIER FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: PCANTAB6 signal peptide; Val at position 1 is most
FEATURE:
OTHER INFORMATION: likely initiator Met.
NAME/KEY: DOMAIN
LOCATION: (23)..(138)
```

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OTHER INFORMATION: 5109 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (139)..(154)
OTHER INFORMATION: 16 amino acid linker.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (155)..(266)
OTHER INFORMATION: 5109 VL domain.
FEATURE:
NAME/KEY: SITE
LOCATION: (270)..(279)
OTHER INFORMATION: myc tag.
FEATURE:
NAME/KEY: SITE
LOCATION: (284)..(289)
OTHER INFORMATION: His tag.
US-09-184-658-63

Query Match      55.6%; Score 800; DB 3; Length 289;
Best Local Similarity 60.3%; Pred. No. 7,2e-57;
Matches 175; Conservative 28; Mismatches 67; Indels 20; Gaps 8;

QY      1  MKYLPTAAGLLLAQAQPAAEVOLVESGGGVVPRPGSLRLSCAASGFTPDYGMNWR 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1  MKKLFLAIPLVPEFYAQAQPAAEVOLVESGGGVVPRPGSLRLSCAASGFTFNTYGMNWR 60

DB
QY      61  QAPGKLEWVSGINMGSGTGYADSVKGRFTISRDNKASLYIQMNSLRADTAIVYCCAR 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61  QTPDKLEWVAITNSNGSLTFYADSVKGRFTISRDNKASLYIQMNSLRADTAIVYCCAR 120

DB
QY      121  MRAPVI-WGGGTLYTVYSRGGSGSGGSGGSGGSSSE--LTQDP-AVSVALGQVTRITCO-- 174
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      121  GYSVYARMGQALVTVSSGGSGSGGSGGSGGSSSDVMTPTPLTSLTITQGSASISCKSS 180

DB
QY      175  -----GDSLSYYASWYQKPGQAPVLIYKNNRPSGIPDRFSGSSSGNTASLTITGAQ 229
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      181  QSLGSDGLT--YLWILQRPQSPKRLIPLVSELDGCVDRFTGSGSGTDFLIKISRAE 238

DB
QY      230  AEDBADYYCNDRDSSGNHV--VFSGGTLTVLGAABQKLISEEDLNGAA 277
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      239  AEDLGVYVC-----CQGTHPPTFGAGTKLE-LKAAAEQKLISEEDLNAAA 283

DB
RESULT 11
US-09-504-262D-63
Sequence 63, Application US/09504262D
Patent No. 6642007
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Saltarelli, Mary J.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
FILE REFERENCE: PC101896GR - CIP of PC9946A
CURRENT APPLICATION NUMBER: US/09/504,262D
EARLIER FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 5109 scFv from clone p5109C scFv7
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL scFv.
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: PCANTAB6 signal peptide; Val at position 1 is most likely initia
OTHER INFORMATION: or Met.
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US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Blazyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646.028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

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Query Match          55.0%; Score 791.5; DB 4; Length 348;
Best Local Similarity 64.1%; Pred. No. 4,4e-56;
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

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QY 23 EVLVVSGGCVVRPGSLRLSCAASGFTPDYKMSVWRQAPKGLEWVSGINMGSTGY 82
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 94 EVLVVSGGCVVRPGSLRLSCAASGFTPDYKMSVWRQAPKGLEWVSGINMGSTGY 153
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 83 ADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARMRAPVY---WGQGLTVTVY-SR 137
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 154 ADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARMRAPVY---WGQGLTVTVY-SR 213
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 138 GGGSGGGSGGGSGGGSG--SETLQDPVAVSVALGQTVRITTCQDLSLR--SYTASWYQKPG 191
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 214 GGGSGGGSGGGSGGGSGSVLTQPSVSAAPGQRVTISCTGSRNSITGAGYDVVMYQKPE 273
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 192 QAPVLVIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPG 251
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 274 TAPKVLIVSNNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPG 333
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 252 GGTKLTVL 259
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 334 GGTKLTVL 341
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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RESULT 15
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Rendly, Brian W.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918.148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75

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Query Match          54.7%; Score 787.5; DB 3; Length 245;
Best Local Similarity 65.2%; Pred. No. 6e-56;
Matches 161; Conservative 28; Mismatches 51; Indels 7; Gaps 4;

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QY 21 MAEVLVESGGGVVRPGSLRLSCAASGFTPDYKMSVWRQAPKGLEWVSGINMGST 80
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DB 1 MAEVLVESGGGVVRPGSLRLSCAASGFTPDYKMSVWRQAPKGLEWVSGINMGST 60
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 81 GYADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARMR---APVWGGTLTVTVYR 137
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 61 YPADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARWSEDAFDYWGQGTMTVTVSS 120
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 138 GGGSGGGSGGGSGGGSG--ELTQDPA--VSVALGQTVRITTCQDLSRYYASWYQKPGQAPV 195
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 121 GGGSGGGSGGGSGGGSDIVMTQSPSTLSASVGRVAITCRASGCIYHMLAMTQKPGAPK 180
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 196 LVIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGQTK 255
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 181 LLIYKASLSLAGAPSRFSGSGGADFTLITSLQPDPAFTYTC--QQYSNYPILTFGGGTR 238
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 256 LTVLGAA 262
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 239 LEYKRAA 245
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Search completed: April 25, 2005, 21:12:13
Job time : 44.6863 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 122.531 Seconds

(without alignment)
752.325 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440
Sequence: 1 MKTLPTAAAGLLLAQPA.....VLGAABQKXSEEDINGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/PTCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppa/PTCTUS_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1440	100.0	277	US-10-032-037B-25	Sequence 25, Appl
2	1440	100.0	277	US-10-029-988B-25	Sequence 25, Appl
3	1440	100.0	277	US-10-032-423A-25	Sequence 25, Appl
4	1440	100.0	277	US-10-029-926B-25	Sequence 25, Appl
5	1416	98.3	277	US-10-032-037B-203	Sequence 203, Appl
6	1416	98.3	277	US-10-029-988B-203	Sequence 203, Appl
7	1416	98.3	277	US-10-032-423A-203	Sequence 203, Appl
8	1416	98.3	277	US-10-029-926B-203	Sequence 203, Appl
9	1388.5	96.4	280	US-10-880-922-6	Sequence 6, Appl
10	1379.5	95.8	280	US-10-880-922-5	Sequence 5, Appl
11	1379.5	95.8	280	US-10-880-922-56	Sequence 56, Appl
12	1378.5	95.7	280	US-10-880-922-60	Sequence 60, Appl
13	1378	95.7	266	US-10-032-037B-204	Sequence 204, Appl

14	1378	95.7	266	US-10-029-988B-204	Sequence 204, Appl
15	1378	95.7	266	US-10-032-423A-204	Sequence 204, Appl
16	1375.5	95.5	280	US-10-880-922-61	Sequence 61, Appl
17	1374.5	95.5	280	US-10-880-922-55	Sequence 55, Appl
18	1294	89.9	291	US-10-406-830-6	Sequence 6, Appl
19	1275.5	88.6	309	US-10-052-798-9	Sequence 9, Appl
20	1275.5	88.6	309	US-10-288-917-9	Sequence 9, Appl
21	1275.5	88.6	309	US-10-423-448-9	Sequence 9, Appl
22	1218.5	84.6	239	US-09-880-748-937	Sequence 937, Appl
23	1218.5	84.6	239	US-10-293-418-937	Sequence 937, Appl
24	1212.5	84.2	239	US-09-880-748-2038	Sequence 2038, Appl
25	1212.5	84.2	239	US-10-293-418-2038	Sequence 2038, Appl
26	1201.5	83.4	230	US-09-969-748C-2	Sequence 2, Appl
27	1201.5	83.4	230	US-09-949-033-2	Sequence 2, Appl
28	1194	82.9	312	US-10-052-798-10	Sequence 10, Appl
29	1194	82.9	312	US-10-288-917-10	Sequence 10, Appl
30	1194	82.9	312	US-10-423-448-10	Sequence 10, Appl
31	1191.5	82.7	239	US-09-880-748-2015	Sequence 2015, Appl
32	1191.5	82.7	239	US-10-293-418-2015	Sequence 2015, Appl
33	1188.5	82.5	236	US-09-969-748C-12	Sequence 12, Appl
34	1188.5	82.5	236	US-09-949-033-75	Sequence 75, Appl
35	1178	81.8	244	US-10-322-673-42	Sequence 42, Appl
36	1139.5	79.1	239	US-09-880-748-2018	Sequence 2018, Appl
37	1139.5	79.1	239	US-10-293-418-2018	Sequence 2018, Appl
38	1133	78.7	244	US-10-322-673-45	Sequence 45, Appl
39	1132.5	78.6	239	US-09-880-748-2035	Sequence 2035, Appl
40	1132.5	78.6	239	US-10-293-418-2035	Sequence 2035, Appl
41	1131.5	78.6	245	US-10-322-673-43	Sequence 43, Appl
42	1131	78.5	252	US-09-880-748-1416	Sequence 1416, Appl
43	1131	78.5	252	US-10-293-418-1416	Sequence 1416, Appl
44	1129.5	78.4	243	US-10-935-290-69	Sequence 69, Appl
45	1127.5	78.3	243	US-09-880-748-2056	Sequence 2056, Appl

ALIGNMENTS

RESULT 1					
US-10-032-037B-25					
Sequence 25, Application US/10032037B					
Publication No. US20040001822A1					
GENERAL INFORMATION:					
APPLICANT: Bio-Technology General Corp.					
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED					
TITLE OR INVENTION: MOETTES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF					
FILE REFERENCE: 10793/44					
CURRENT APPLICATION NUMBER: US/10/032,037B					
CURRENT FILING DATE: 2001-12-31					
PRIOR APPLICATION NUMBER: 60/258,948					
PRIOR FILING DATE: 2000-12-29					
NUMBER OF SEQ ID NOS: 204					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 25					
LENGTH: 277					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-10-032-037B-25					
Query Match					
Best Local Similarity 100.0%; Score 1440; DB 15; Length 277;					
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	1	1	1	1
DB	1	1	1	1	1
QY	61	QABGKLEWVSGINWNGSTGVYDSYKGRFTTSRDNAKSLYVQNMSLRDEPAVYYCAR	120		
DB	61	QABGKLEWVSGINWNGSTGVYDSYKGRFTTSRDNAKSLYVQNMSLRDEPAVYYCAR	120		
QY	121	MRAPVIMGGQTLVTVSRGGGSGGGSGGGSGGSELTPDPAVSVYALGQTVRITCGDSLRS	180		
DB	121	MRAPVIMGGQTLVTVSRGGGSGGGSGGGSGGSELTPDPAVSVYALGQTVRITCGDSLRS	180		

QY 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240

QY 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277

RESULT 2
US-10-029-988B-25

; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25

; LENGTH: 277
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match 100.0%; Score 1440; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLLPTAAGLLILAAQPMABEVQLVESGGGVYRRPGSIRLSCASGTFPDYGMSSWR 60
DB 1 MKTLLPTAAGLLILAAQPMABEVQLVESGGGVYRRPGSIRLSCASGTFPDYGMSSWR 60

QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120

QY 121 MRAPVIMGGTTLTVTRSGGSGSGGSSSELTQDPAVSVVALGQTVRITCGDSLSRS 180
DB 121 MRAPVIMGGTTLTVTRSGGSGSGGSSSELTQDPAVSVVALGQTVRITCGDSLSRS 180

QY 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240

QY 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277

RESULT 3
US-10-032-423A-25

; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match 100.0%; Score 1440; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLLPTAAGLLILAAQPMABEVQLVESGGGVYRRPGSIRLSCASGTFPDYGMSSWR 60
DB 1 MKTLLPTAAGLLILAAQPMABEVQLVESGGGVYRRPGSIRLSCASGTFPDYGMSSWR 60

QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120

QY 121 MRAPVIMGGTTLTVTRSGGSGSGGSSSELTQDPAVSVVALGQTVRITCGDSLSRS 180
DB 121 MRAPVIMGGTTLTVTRSGGSGSGGSSSELTQDPAVSVVALGQTVRITCGDSLSRS 180

QY 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240

QY 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277

RESULT 4
US-10-029-926B-25

; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:

; APPLICANT: HAGAY, et al
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25

; LENGTH: 277
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match 100.0%; Score 1440; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLLPTAAGLLILAAQPMABEVQLVESGGGVYRRPGSIRLSCASGTFPDYGMSSWR 60
DB 1 MKTLLPTAAGLLILAAQPMABEVQLVESGGGVYRRPGSIRLSCASGTFPDYGMSSWR 60

QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120

QY 121 MRAPVIMGGTTLTVTRSGGSGSGGSSSELTQDPAVSVVALGQTVRITCGDSLSRS 180
DB 121 MRAPVIMGGTTLTVTRSGGSGSGGSSSELTQDPAVSVVALGQTVRITCGDSLSRS 180

QY 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YVASWTQOKFGQAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240

QY 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAABEQKLISEBDLNGAA 277

RESULT 5
US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2,6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGSIRLSCAASGFTFDDYGMWVR 60
DB 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGSIRLSCAASGFTFDDYGMWVR 60
QY 61 QAPGKGLIEWSGINMNGSTGVADSVKGRFTISRDNKNSLYIQMNSLRADPAVYYCAR 120
DB 61 QAPGKGLIEWSGINMNGSTGVADSVKGRFTISRDNKNSLYIQMNSLRADPAVYYCAR 120
QY 121 MRAPVWGQGLTVTVSRGGSGSGGSSSELTDDPAVSVALGQTVRITCGDSLRS 180
DB 121 LTHPYFGQGLTVTVSRGGSGSGGSSSELTDDPAVSVALGQTVRITCGDSLRS 180
QY 181 YVASWYQQRKQAPVLYVYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
DB 181 YVASWYQQRKQAPVLYVYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
QY 241 RDSSGNHVVFGGTTKLTVLGAQAEQKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGTTKLTVLGAQAEQKLISEEDLNGAA 277

RESULT 6
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2,6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGSIRLSCAASGFTFDDYGMWVR 60

DB 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGSIRLSCAASGFTFDDYGMWVR 60
QY 61 QAPGKGLIEWSGINMNGSTGVADSVKGRFTISRDNKNSLYIQMNSLRADPAVYYCAR 120
DB 61 QAPGKGLIEWSGINMNGSTGVADSVKGRFTISRDNKNSLYIQMNSLRADPAVYYCAR 120
QY 121 MRAPVWGQGLTVTVSRGGSGSGGSSSELTDDPAVSVALGQTVRITCGDSLRS 180
DB 121 LTHPYFGQGLTVTVSRGGSGSGGSSSELTDDPAVSVALGQTVRITCGDSLRS 180
QY 181 YVASWYQQRKQAPVLYVYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
DB 181 YVASWYQQRKQAPVLYVYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
QY 241 RDSSGNHVVFGGTTKLTVLGAQAEQKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGTTKLTVLGAQAEQKLISEEDLNGAA 277

RESULT 7
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2,6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGSIRLSCAASGFTFDDYGMWVR 60
DB 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGSIRLSCAASGFTFDDYGMWVR 60
QY 61 QAPGKGLIEWSGINMNGSTGVADSVKGRFTISRDNKNSLYIQMNSLRADPAVYYCAR 120
DB 61 QAPGKGLIEWSGINMNGSTGVADSVKGRFTISRDNKNSLYIQMNSLRADPAVYYCAR 120
QY 121 MRAPVWGQGLTVTVSRGGSGSGGSSSELTDDPAVSVALGQTVRITCGDSLRS 180
DB 121 LTHPYFGQGLTVTVSRGGSGSGGSSSELTDDPAVSVALGQTVRITCGDSLRS 180
QY 181 YVASWYQQRKQAPVLYVYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
DB 181 YVASWYQQRKQAPVLYVYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
QY 241 RDSSGNHVVFGGTTKLTVLGAQAEQKLISEEDLNGAA 277
DB 241 RDSSGNHVVFGGTTKLTVLGAQAEQKLISEEDLNGAA 277

RESULT 8
US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY

FILE REFERENCE: 10793/50
 CURRENT APPLICATION NUMBER: US/10/029,926B
 CURRENT FILING DATE: 2001-12-31
 PRIOR APPLICATION NUMBER: 60/258,948
 PRIOR FILING DATE: 12/29/2000
 NUMBER OF SEQ ID NOS: 203
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 203
 LENGTH: 277
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-029-926B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
 Best Local Similarity 98.2%; Pred. No. 2,6e-88;
 Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 60
 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 60
 DB 61 QAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYYCAR 120
 61 QAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYYCAR 120
 QY 121 MRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 180
 121 LHPYRMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 180
 DB 181 YVASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
 181 YVASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
 QY 241 RDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277
 241 RDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277
 DB 241 RDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277

RESULT 9
 US-10-880-922-6
 Sequence 6, Application US/10880922
 Publication No. US20050069955A1
 GENERAL INFORMATION:
 APPLICANT: PLAKSIN, DANIEL
 APPLICANT: LEVANON, AVIGDOR
 APPLICANT: SZANTON, ESTHER
 APPLICANT: HAGAY, YOCHAVED
 APPLICANT: BEN-LEVY, RACHEL
 APPLICANT: NISGAV, YAEEL
 APPLICANT: KANFI, YARIV
 TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
 FILE REFERENCE: 10793-143
 CURRENT APPLICATION NUMBER: US/10/880,922
 CURRENT FILING DATE: 2004-06-30
 PRIOR APPLICATION NUMBER: 60/484,061
 PRIOR FILING DATE: 2003-06-30
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: Patent In Ver. 3.2
 SEQ ID NO 6
 LENGTH: 280
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: consensus antibody
 US-10-880-922-6

Query Match 96.4%; Score 1388.5; DB 17; Length 280;
 Best Local Similarity 96.8%; Pred. No. 1.9e-86;
 Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 57
 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 57

DB 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 60
 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 60
 QY 58 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 117
 58 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 117
 DB 61 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 120
 61 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 120
 QY 118 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 177
 118 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 177
 DB 121 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 180
 121 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 180
 QY 178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237
 178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237
 DB 181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240
 181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240
 QY 238 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277
 238 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277
 DB 241 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 280
 241 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 280

RESULT 10
 US-10-880-922-5
 Sequence 5, Application US/10880922
 Publication No. US20050069955A1
 GENERAL INFORMATION:
 APPLICANT: PLAKSIN, DANIEL
 APPLICANT: LEVANON, AVIGDOR
 APPLICANT: SZANTON, ESTHER
 APPLICANT: HAGAY, YOCHAVED
 APPLICANT: BEN-LEVY, RACHEL
 APPLICANT: NISGAV, YAEEL
 APPLICANT: KANFI, YARIV
 TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
 FILE REFERENCE: 10793-143
 CURRENT APPLICATION NUMBER: US/10/880,922
 CURRENT FILING DATE: 2004-06-30
 PRIOR APPLICATION NUMBER: 60/484,061
 PRIOR FILING DATE: 2003-06-30
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: Patent In Ver. 3.2
 SEQ ID NO 5
 LENGTH: 280
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: consensus antibody
 US-10-880-922-5

Query Match 95.8%; Score 1379.5; DB 17; Length 280;
 Best Local Similarity 96.1%; Pred. No. 7.7e-86;
 Matches 269; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 57
 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 57
 DB 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 60
 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGGSLRLSCAASGFTDDYGMYSWR 60
 QY 58 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 117
 58 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 117
 DB 61 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 120
 61 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRAREDYAVYY 120
 QY 118 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 177
 118 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 177
 DB 121 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 180
 121 CARMRAPVIMGGTLTVTSRGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQSDS 180
 QY 178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237
 178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237
 DB 181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240
 181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240
 QY 238 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277
 238 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 277
 DB 241 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 280
 241 CNSRDSGNNHVVFGGKTLTVLGAABEQKLISEEDLNGAA 280

RESULT 11
US-10-880-922-56
; Sequence 56, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANTON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHAVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YAEI
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 56
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-880-922-56

Query Match 95.8%; Score 1379.5; DB 17; Length 280;
Best Local Similarity 95.7%; Pred. No. 7, 7e-86;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;
QY 1 MKTLPPTAAGLLLLAOPMAEVQVLESQGGVVRPGSIRLSCASGFTFDLNPVKYM 57
1 MKTLPPTAAGLLLLAOPMAEVQVLESQGGVVRPGSIRLSCASGFTFDLNPVKYM 60
DB 58 WVRQAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRABEDTAVYY 117
61 WVRQAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRABEDTAVYY 120
QY 118 CARMRAPIWGGTTLVTSRGGSGGSGSSSELTQDPAVSVALGQTVRITTCQGS 177
121 CARLRPPFLWGGTTLVTSRGGSGGSGGSSSELTQDPAVSVALGQTVRITTCQGS 180
DB 178 LRSYASWYQOKRQAPVLYVYGNRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237
181 LRSYASWYQOKRQAPVLYVYGNRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240
QY 238 CNSRDSSGNHVFVGGGKTLTVLGAABEQKLISEEDLNGAA 277
241 CNSRDSSGNHVFVGGGKTLTVLGAABEQKLISEEDLNGAA 280
DB

RESULT 12
US-10-880-922-60
; Sequence 60, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANTON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHAVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YAEI
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 60
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-880-922-60

Query Match 95.7%; Score 1378.5; DB 17; Length 280;
Best Local Similarity 95.7%; Pred. No. 9e-86;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;
QY 1 MKTLPPTAAGLLLLAOPMAEVQVLESQGGVVRPGSIRLSCASGFTFDLNPVKYM 57
1 MKTLPPTAAGLLLLAOPMAEVQVLESQGGVVRPGSIRLSCASGFTFDLNPVKYM 60
DB 58 WVRQAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRABEDTAVYY 117
61 WVRQAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRABEDTAVYY 120
QY 118 CARMRAPIWGGTTLVTSRGGSGGSGSSSELTQDPAVSVALGQTVRITTCQGS 177
121 CARLRPPFLWGGTTLVTSRGGSGGSGGSSSELTQDPAVSVALGQTVRITTCQGS 180
DB 178 LRSYASWYQOKRQAPVLYVYGNRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237
181 LRSYASWYQOKRQAPVLYVYGNRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240
QY 238 CNSRDSSGNHVFVGGGKTLTVLGAABEQKLISEEDLNGAA 277
241 CNSRDSSGNHVFVGGGKTLTVLGAABEQKLISEEDLNGAA 280
DB

RESULT 13
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKTLPPTAAGLLLLAOPMAEVQVLESQGGVVRPGSIRLSCASGFTFDLNPVKYM 60
1 MKTLPPTAAGLLLLAOPMAEVQVLESQGGVVRPGSIRLSCASGFTFDLNPVKYM 60
DB 61 QAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRABEDTAVYYCAR 120
QY 121 MRAPVYWGCGTTLVTSRGGSGGSGSSSELTQDPAVSVALGQTVRITTCQGSLS 180
121 MRAPVYWGCGTTLVTSRGGSGGSGSSSELTQDPAVSVALGQTVRITTCQGSLS 180
DB 121 MRAPVYWGCGTTLVTSRGGSGGSGSSSELTQDPAVSVALGQTVRITTCQGSLS 180
181 YVASWYQOKRQAPVLYVYGNRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

Db 181 YYASWYQKRGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
QY 241 RDSSGNHVVFGGKTTLVLAAGAAEOK 266
Db 241 RDSSGNHVVFGGKTTLVLAAGAAKAK 266

RESULT 14

US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOLETTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAOPMAEVOVLESQGVVRPGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAOPMAEVOVLESQGVVRPGSLRLSCAASGFTFDDYGMWVR 60
QY 61 QAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIVYYCAR 120
Db 61 QAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIVYYCAR 120
QY 121 MRAPVIMGGTILVTVSRGGSGSGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180
Db 121 MRAPVIMGGTILVTVSRGGSGSGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180
QY 181 YYASWYQKRGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
Db 181 YYASWYQKRGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
QY 241 RDSSGNHVVFGGKTTLVLAAGAAEOK 266
Db 241 RDSSGNHVVFGGKTTLVLAAGAAKAK 266

RESULT 15

US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOLETTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAOPMAEVOVLESQGVVRPGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAOPMAEVOVLESQGVVRPGSLRLSCAASGFTFDDYGMWVR 60
QY 61 QAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIVYYCAR 120
Db 61 QAPGKLEWVSGINMNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIVYYCAR 120
QY 121 MRAPVIMGGTILVTVSRGGSGSGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180
Db 121 MRAPVIMGGTILVTVSRGGSGSGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180
QY 181 YYASWYQKRGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
Db 181 YYASWYQKRGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
QY 241 RDSSGNHVVFGGKTTLVLAAGAAEOK 266
Db 241 RDSSGNHVVFGGKTTLVLAAGAAKAK 266

Search completed: April 25, 2005, 21:09:47
Job time : 122.531 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: April 25, 2005, 19:57:16 ; Search time 31.9379 Seconds
(without alignments)

834.495 Million cell updates/sec

Title: US-10-029-926d-25

Perfect score: 1440

Sequence: 1 MKYLPTAAAGLLLLAQA.....VLGAAGQKLISEEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643.5	44.7	268	A56446	Ig heavy chain V r
2	568	39.4	109	S19663	Ig lambda chain V
3	565.5	39.3	249	S41374	single chain Fv an
4	562	39.0	108	S47184	Ig lambda chain -
5	551.5	38.3	110	S36272	Ig lambda chain V
6	546	37.9	127	S70444	Ig lambda chain pr
7	541	37.6	108	S38498	Ig lambda chain -
8	539	37.4	109	S38496	Ig lambda chain -
9	530.5	36.8	233	S25748	Ig lambda chain -
10	527	36.6	108	L3HUSH	Ig lambda chain V-
11	522.5	36.3	233	JCS322	p53 specific singl
12	518.5	36.0	110	S19672	Ig lambda chain V-
13	518	35.6	146	S02083	Ig lambda chain V-
14	513	35.6	98	S26928	Ig heavy chain V r
15	510.5	35.5	128	S31595	Ig heavy chain V r
16	503	34.9	96	S36060	Ig lambda chain -
17	503	34.9	115	S13726	Ig lambda chain -
18	503	34.9	121	S31118	Ig heavy chain - h
19	502.5	34.9	233	S25741	Ig lambda chain -
20	502	34.9	123	S30532	Ig heavy chain V r
21	501	34.8	121	S31104	Ig heavy chain (su
22	495.5	34.4	112	PH1654	Ig heavy chain V r
23	491	34.1	120	S36273	Ig heavy chain V r
24	489.5	34.0	145	S11239	Ig heavy chain V r
25	489	33.9	134	S31699	Ig heavy chain V r
26	488	33.8	138	S31666	Ig heavy chain V r
27	486	33.7	160	S05271	Ig heavy chain pre
28	485.5	33.7	120	S44111	Ig heavy chain V-D
29	485	33.7	119	S31108	Ig heavy chain - h

30	484.5	33.6	120	2	S48798	Ig heavy chain V r
31	482	33.5	119	2	S31107	Ig heavy chain - h
32	480	33.3	121	2	I55673	Ig heavy chain - h
33	480	33.3	123	2	S31114	Ig heavy chain - h
34	478	33.2	119	2	D36005	Ig heavy chain V r
35	478	33.2	140	2	S31686	Ig heavy chain V r
36	477	33.1	139	2	I37781	Ig variable region
37	476	33.1	119	2	C36005	Ig heavy chain V r
38	474.5	33.0	140	2	S70442	Ig heavy chain pre
39	474.5	33.0	147	2	I37780	Ig variable region
40	474.5	33.0	151	2	A60943	Ig heavy chain pre
41	474	32.9	135	2	S31598	Ig heavy chain V r
42	473.5	32.9	124	2	S20782	Ig heavy chain V r
43	473.5	32.9	128	2	S26790	Ig heavy chain V r
44	473	32.8	127	2	S38489	Ig heavy chain - h
45	472	32.8	98	2	S26927	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 44.7%; Score 643.5; DB 2; Length 268;

Best Local Similarity 51.3%; Pred. NO. 4.4e-36;

Matches 139; Conservative 35; Mismatches 80; Indels 17; Gaps 6;

QY	21	MAEVLVESGGGVVPRGSGRLSCAASGFTPDYGMHWQAQPGLEWYSGINWGSGT	80
DB	1	MAQVKLOESGAEIVKGCASVKTCTSGFRIKDTVMHWYQRPQGLFWIGRIAPANGIT	60
QY	81	GYADSVKGRFTISRDNKNSLYIQMNSLRADDTAVYYCAR--MRAPIWGQGLTVTSR	137
DB	61	KYDPKFGKATIAADTSNMTAVYLQSLTSEDTAVYYCASVYLTRYENWYQGQTVTVSS	120
QY	138	GGGSGGGSGGGSGGSS-ELTQDPVAV--SVALGQVVRITCGDSLRSTYASRYQKPGQAPV	195
DB	121	GGGSGGGSGGGSGGSDIELQSPAIMSASISGEIVTSCRASSSVN--FIYYQDKSDSPK	179
QY	196	LVIYVKKNRPSGIPDRFGSSSGNTASLTITGAQAEADYVNCNRSRDSGNHVPFGGQT	255
DB	180	LMVYITSHLPVGPVPAFSGSGSGNSYSLTISMEGEDAITYCOQPTSS--PFTFGSGTK	237
QY	256	LTVLGA-----AAGQKLISEEDLNGAA 277	
DB	238	LEIKRMAHHHHHGAAGQKLISEEDLNGAA 268	

RESULT 2

S19663 Ig lambda chain V region (clone alpha-B9A3) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19663

R/Marke, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19663
 A/Molecule type: mRNA
 A/Residues: 1-109 <MCI>
 A/Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:91340166
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 568; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.9e-31;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 211
 DB 1 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 60
 QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGSGTKLTVLG 260
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGSGTKLTVLG 109

RESULT 3

S41374
 Ig lambda chain Fv antibody - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C/Accession: S41374
 R/Artsemenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.
 Submitted to the EMBL Data Library, January 1994
 A/Description: Construction and functional characterization of a single chain Fv antibody
 A/Reference number: S41374
 A/Accession: S41374
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-249 <ART>
 A/Cross-references: EMBL:Z29480

Query Match 39.3%; Score 565.5; DB 2; Length 249;
 Best Local Similarity 48.2%; Pred. No. 6.5e-31;
 Matches 123; Conservative 37; Mismatches 74; Indels 21; Gaps 6;

QY 23 EVOLVESGGVVPGGSLRLSCAAGTTPDDYGNKSWRQAPKGLKLEWVSGINMGSTGY 82
 DB 1 OVALOOSGALVLRPGASVSKLCTASGFNFDDYIHVKQRPKLEWIAIAPASGVNKY 60
 QY 83 ADVKGRFTISRNKXSKYLQMSLAEDTAVYYCAR---KRAPIYKOGTLTYMSRG 138
 DB 61 VPRFDQATTTADTSSNTAYLLSLTSEDTAVYYCARDDLTYSLGWQSGSTVTVSSR 120
 QY 139 GGGSGGGSGGGSS-ELTOD-PAVSVALGQTVRITCO-----GDSLSRYASWYQ 187
 DB 121 GGGSGGGSGGGSDIELTOSPSVVIYIPGSVISICRSKSLYSDGS-----YLFWFL 176
 QY 188 QKPGQAPVLVIYGNKPPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNN 247
 DB 177 QRRGQSPQLIYRMSNLASGVPRFSGSGSTFTLRISVKEADYGVVYCMQHR--YP 234
 QY 248 VVFGGTKLTVLGA 262
 DB 235 LTFGAGTKLEIKRA 249

RESULT 4

S47184
 Ig lambda chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S47184
 R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
 Submitted to the EMBL Data Library, June 1994
 A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
 A/Reference number: S47181
 A/Accession: S47184

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-108 <MCI>
 A/Cross-references: EMBL:X79783; NID:g506426; PIDN:CA56179.1; PID:g506427
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 562; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.7e-31;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 211
 DB 1 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 60
 QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGSGTKLTVL 259
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGSGTKLTVL 108

RESULT 5

S36272
 Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 C/Accession: S36272
 R/Griffiths, A.D.; Malngvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBD U. 12, 725-734, 1993
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.
 A/Reference number: S36256; M0ID:93178448; PMID:7679990
 A/Accession: S36272
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-110 <GRI>
 A/Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g933912
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 551.5; DB 2; Length 110;
 Best Local Similarity 98.2%; Pred. No. 2.4e-30;
 Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 152 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 211
 DB 1 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 60
 QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGSGTKLTVLG 260
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVVGSGTKLTVLG 110

RESULT 6

S70444
 Ig lambda chain precursor V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C/Accession: S70444; S70426
 R/Crisp, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
 Mol. Immunol. 29, 1363-1373, 1992
 A/Title: Igm kappa/lambda BBV human B cell clone: an early step of differentiation of B
 A/Reference number: S70442; M0ID:93024508; PMID:1383695
 A/Accession: S70444
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-127 <CUI>
 A/Cross-references: UNIPROT:Q9NSD6
 A/Experimental source: clone E29.1
 R/Tonnelie, C.
 Submitted to the EMBL Data Library, May 1990
 A/Reference number: S70426
 A/Accession: S70426

A:Molecule type: mRNA
 A:Residues: 1-90 <TON>
 A:Cross-references: EMBL:X53070
 A:Experimental source: cell line E29.1, clone VL 29-1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
 F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 37.8%; Score 546; DB 2; Length 127;
 Best Local Similarity 97.2%; Pred. No. 6.5e-30;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 211
 DB 20 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 79

QY 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 259
 DB 80 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 127

RESULT 7
 S38498
 Ig lambda chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_rev15ion 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S38498
 R/Mark: J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.
 submitted to the EMBL Data Library, June 1993
 A:Description: Human antibody fragments specific for human blood group antigens from a P
 A:Reference number: S38488
 A:Accession: S38498
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <NAR>
 A:Cross-references: EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; PID:G414044
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F/14-88/Domain: immunoglobulin homology <IMM>

Query Match 37.6%; Score 541; DB 2; Length 108;
 Best Local Similarity 97.2%; Pred. No. 1.2e-29;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 153 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 212
 DB 1 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 213 SSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 260
 DB 61 SSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 108

RESULT 8
 S38496
 Ig lambda chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_rev15ion 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S38496
 R/Mark: J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S.
 submitted to the EMBL Data Library, June 1993
 A:Description: Human antibody fragments specific for human blood group antigens from a P
 A:Reference number: S38488
 A:Accession: S38496
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <NAR>
 A:Cross-references: EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PID:G414040
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 37.4%; Score 539; DB 2; Length 109;
 Best Local Similarity 93.6%; Pred. No. 1.6e-29;
 Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 211
 DB 1 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 260
 DB 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 109

RESULT 9
 S25748
 Ig lambda chain - human
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_rev15ion 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S25748
 R/Comblato, G.; Klobeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A>Title: V(Lambda) and J(Lambda) gene segments of the human immunoglobulin la
 A:Reference number: S16439; PMID:91257162; PMID:1904362
 A:Accession: S25748
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-233 <COM>
 A:Cross-references: EMBL:X57813; NID:G33725; PIDN:CAA0950.1; PID:G33726
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F/148-216/Domain: immunoglobulin homology <IMM>

Query Match 36.8%; Score 530.5; DB 2; Length 233;
 Best Local Similarity 83.5%; Pred. No. 1.3e-28;
 Matches 106; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

QY 152 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 211
 DB 20 SSELTDPAVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 79

QY 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 268
 DB 80 FSGSSSGNTASLTITGAQAEADYYCNSRDSGNHVFGGCTKLTVL 139

QY 269 --SEEDL 273
 DB 140 PPSSEEL 146

RESULT 10
 L3H0SH
 Ig lambda chain V-III region (Sh) - human
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_rev15ion 24-Apr-1984 #text_change 09-Jul-2004
 C/Accession: A01980
 R/Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
 J. Biol. Chem. 245, 2171-2176, 1970
 A>Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complet
 A:Reference number: A92057; PMID:70166723; PMID:4909564
 A:Accession: A01980
 A:Molecule type: protein
 A:Residues: 1-108 <RTT>
 A:Cross-references: UNIPROT:P01714
 A>Note: the sequence of the C region is also given
 C:Genetics:
 A:Gene: GDB:119342; OMIM:147240
 A:Cross-references: GDB:119342; OMIM:147240
 A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

QY 83 ADSVKGRFTISRDNKNSLYLQWNSLRAPDTAVYYCAR 120
 |||||
 Db 61 ADSVKGRFTISRDNKNSLYLQWNSLRAPDTALYHCAR 98
 |||||

RESULT 15

S31595
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31595
 R:Clisnier, A.W.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31595
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-128 <CUI>
 A:Cross-references: EMBL:Z14171; NID:G31007; PIDN:CA78540.1; PID:G31008
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:23-106/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 510.5; DB 2; Length 128;
 Best Local Similarity 83.3%; Pred. No. 1.5e-27;
 Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
 QY 23 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMNWVROAPKGLEWVSGINWNGSGTGY 82
 |||||:|||||
 Db 9 EVOLVESGGGLVQPGKSLRLSCAASGFTPDYAMHWVROAPKGLEWVSGISWNSGSIgy 68
 |||||:|||||
 QY 83 ADSVKGRFTISRDNKNSLYLQWNSLRAPDTAVYYCARMAP-----VWGGGTLYTVS 136
 |||||:|||||
 Db 69 ADSVKGRFTISRDNKNSLYLQWNSLRAPDTALYHCAR-DAPGDHDAFDIWGGTMYTVS 127
 |||||:|||||

Search completed: April 25, 2005, 20:24:08
 Job time : 31.9379 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 143.106 seconds
(without alignments)
991.192 Million cell updates/sec

Title: US-10-029-926D-25
Perfect score: 1440
Sequence: 1 MKYLLPTAAGLLLAQPA.....VLGAAGKLISEEDINGAA 277

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	52.6	240	2	065ZC9 065ZC9 homo sapien
2	723.5	50.2	298	2	09QYF0 09QYF0 synthetic c
3	715	49.7	255	2	06K805 06K805 mus musculu
4	693.5	48.3	248	2	065ZQ7 065ZQ7 mus sp. b31
5	636	44.2	244	2	065ZC8 065ZC8 homo sapien
6	600	41.7	241	2	0921A6 0921A6 mus musculu
7	578	40.1	243	2	07TOM2 07TOM2 mus musculu
8	552	38.3	107	2	09NSD6 09NSD6 homo sapien
9	550.5	38.2	112	2	09HCC1 09HCC1 homo sapien
10	548	38.1	487	2	065ZL2 065ZL2 mus sp. fv/
11	530	36.8	233	2	06GMW4 06GMW4 homo sapien
12	527	36.6	108	1	LV3A HUMAN F01714 homo sapien
13	516	35.8	472	2	08N0B9 08N0B9 homo sapien
14	511	35.5	499	2	08NSK4 08NSK4 homo sapien
15	508	35.3	573	2	08WU38 08WU38 homo sapien
16	507.5	35.2	218	2	0925S1 0925S1 mus musculu
17	483	33.5	121	2	09UL71 09UL71 homo sapien
18	478	33.2	470	2	06PJ44 06PJ44 homo sapien
19	478	33.2	478	2	06PI81 06PI81 homo sapien
20	477	33.1	606	2	06GMW2 06GMW2 homo sapien
21	474	32.9	464	2	06MZU6 06MZU6 homo sapien
22	474	32.9	613	2	08WUK1 08WUK1 homo sapien
23	473.5	32.9	497	2	096BB9 096BB9 homo sapien
24	471.5	32.7	473	2	06MZV7 06MZV7 homo sapien
25	470	32.6	113	2	09UL90 09UL90 homo sapien
26	465	32.3	493	2	06GMK2 06GMK2 homo sapien
27	461.5	32.0	118	2	09UL91 09UL91 homo sapien
28	457.5	31.8	475	2	06MZQ6 06MZQ6 homo sapien
29	456	31.7	466	2	06IN78 06IN78 homo sapien
30	452.5	31.4	479	2	06MZV6 06MZV6 homo sapien
31	450	31.2	473	2	091Z05 091Z05 mus musculu

32	448.5	31.1	465	2	06PE64 06PE64 homo sapien
33	446.5	31.0	116	1	HV3T HUMAN P01781 homo sapien
34	446.5	31.0	494	2	06ZW64 06ZW64 homo sapien
35	445	30.9	479	2	091WP5 091WP5 mus musculu
36	444.5	30.9	122	1	HV3E HUMAN P01768 homo sapien
37	444	30.8	116	2	09UL93 09UL93 homo sapien
38	443	30.8	117	1	HV3C HUMAN P01764 homo sapien
39	441.5	30.7	494	2	096K68 096K68 homo sapien
40	440.5	30.6	483	2	06MX9 06MX9 homo sapien
41	440	30.6	485	2	06PDB8 06PDB8 mus musculu
42	439.5	30.5	544	2	06PJ95 06PJ95 homo sapien
43	439	30.5	480	2	06N094 06N094 homo sapien
44	436.5	30.3	118	2	09UL72 09UL72 homo sapien
45	436.5	30.3	475	2	06GMW7 06GMW7 homo sapien

ALIGNMENTS

RESULT 1					
ID	065ZC9	PRELIMINARY:	PRT:	240 AA.	
AC	065ZC9				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)				
DE	Single-chain Fv (Fragment).				
GN	Name=scFv;				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
NCBI	TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C1q/7;				
RX	MEDLINE=97362799; PubMed=9219263;				
RA	Kontermann R.E., Wing M.G., Winter G.;				
RT	"Complement recruitment using bispecific diabodies.";				
RL	Nat. Biotechnol. 15:629-631(1997).				
DR	EMBL; Y13056; CAA73499.1; -.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_2.				
DR	SMART; SM00409; Ig_2.				
DR	SMART; SM00406; IgV_2.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
FT	NON TER 1				
FT	NON TER 240				
SQ	SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;				
Query Match 52.6%; Score 758; DB 2; Length 240;					
Best local Similarity 62.9%; Pred. No. 1.7e-46;					
Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;					
QY	23 EVLVESGGGVPRGSLRLSCAAGFTDDYGMVWROAPGKLEWVGIMNGSTGY 82				
DB	1 QVQLVQSGGGLVPGGSLRLSCAAGFTSSYGMAHWROAPGKLEWVAITSDSNKTY 60				
QY	83 ADSVKRFTISRDNAKNSLYLNQNSLRADDAVYVCARRAPVY--WGQTLTVRSGG 140				
DB	61 ADSVKRFTISRDNAKNSLYLNQNSLRADDAVYVCARRAPVY--WGQTLTVRSGG 120				
QY	141 GSGGGSGGGSGS-ELTQDPA--VSVALGQTVRTCCGDSLRYSYASWYQKPGQAPLV 198				
DB	121 GSGGGSGGGSGSDIQWTQSPSTLSASIGDRVITTCRASBGIVRWLAWYQKPGKAPLV 180				
QY	199 YGKNRNPSPGIPRFSGSSSGNTASLTITGAQADEADYVCNSRDSGNTVVEGGRKLV 258				
DB	181 YKASLASAPAPSFSGSGGTPTLTITSLQPDPAFYVC--QQYSNPVLRGGKLV 238				

090YFO PRELIMINARY; PRT; 298 AA.

AC 090YFO; 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)

DE CN 8 single chain antibody.

GN Name=CN 8 scFv;

OS synthetic construct.

OC other sequences: artificial sequences.

OX NCBI_TaxID=32630;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;

RA Shihbata N., Demura T., Fukuda H.;

RT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phase display subtraction method."

RT Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

RL EMBL; AB036341; BAA8633.1; -.

DR PIR; A33933; A33933.

DR PIR; S19112; S19112.

DR HSSP; P01820; 1A70.

DR InterPro; IPR007110; Ig_1like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PSS0835; IG LIKE; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 50.2%; Score 723.5; DB 2; Length 298;

Best Local Similarity 57.0%; Pred. No. 6.2e-44;

Matches 147; Conservative 28; Mismatches 66; Indels 17; Gaps 5;

QY 16 AAGPAAAEVQLVSSGGGVPRGSLRLSCAAGTTPDYGMWVROAPGKLEWVSGINM 75

DB 33 AAGPAAAEVQLVSSGGGVPRGSLRLSCAAGTTPDYGMWVROAPGKLEWVSGINP 92

QY 76 NGSTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYICARMR---APYIWGGTL 132

DB 93 DSSTINTVPSLKNKFTISRDNKNTLYLQMSKVRSEDTALYICARASYGHSAYWGQGT 152

QY 133 VTVSRGGSGGGSGGGSGSSS-ELTQDP-AVSVALGQTVRITQGDLSRYASWYQOKP 190

DB 153 VTVSSGGSGGGSGGGSGGSDIELTQSPASLSAVGETVITTCRASGNINHYLAWYQOKQ 212

QY 191 GQAPVLYIVYGKNNRPSGIPDRFGSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNF--- 247

DB 213 GKSPQLLVYNAKTLADVPSPFGSGSGTQYSLKINSLQPEDFGSYTC-----QHFWT 265

QY 248 --VVFSGGTGLTVLGAA 263

DB 266 TPYTFGGGTLEIKRAA 283

RESULT 3

Q6KB05 PRELIMINARY; PRT; 255 AA.

AC 06KB05; 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)

DE SCFV B8E5 protein (Fragment).

GN Name=scFv B8E5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=Balb/c;

RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,

RA Briand J.P., Hoebeke J.;

RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ746180; CAG34081.1; -.

DR HSSP; P01837; 1KCR.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig_1like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00409; IGV; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PSS0835; IG LIKE; 2.

FT NON TER 1

SQ SEQUENCE 255 AA; 27445 MW; B6BBD38395DFF13B CRC64;

Query Match 49.7%; Score 715; DB 2; Length 255;

Best Local Similarity 58.8%; Pred. No. 2.1e-43;

Matches 147; Conservative 33; Mismatches 54; Indels 16; Gaps 6;

QY 23 EVOLVBSGGGVPRGSLRLSCAAGTTPDYGMWVROAPGKLEWVSGINMGSTGY 82

DB 1 QVQLQSGDVLVPGGSLKLVSCAAGFTISSTGMWVROTPDKRLKLEWVAITISGSGSYTY 60

QY 83 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYICARM-----RAPYIWGGTLVTVS 136

DB 61 PDSVKGRFTISRDNKNTLYLQMSKVRSEDTALYICARHINRYDGAFFYWGQGTLLTVS 120

QY 137 RGGGSGGGSGGGSGSSS-ELTQDP-AVSVALGQTVRITQGDLS-----RSTYASWYQO 188

DB 121 SCGGSGSGGGSGGGSGGSDIWAQSPSSLSVAGKRVIMSCSSQSLSNRSRQKRYLAWYQO 180

QY 189 KPGQAEVLYIVYGKNNRPSGIPDRFGSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNF 248

DB 181 KPQGSPLLYLGASTRESGVPRFTSGSGTDEFTLITSSVQAEADLAIVLCQNDHS--YFL 238

QY 249 VFGSGTGLTV 258

DB 239 TFGAGTKLEI 248

RESULT 4

Q65Z07 PRELIMINARY; PRT; 248 AA.

AC 065Z07; 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, last annotation update)

DE B3 (Fv)-PE40 (Fragment).

GN Name=B3 (Fv)-PE40;

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92020904; PubMed=1924323;

RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Paetan I.;

RT "B3 (Fv)-PE38KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice."

RT Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).

RL EMBL; S57990; AAB19971.2; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig_1like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; IGV; 2.

DR SMART; SM00409; IGV; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PSS0835; IG LIKE; 2.

FT NON TER 248

SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 48.3%; Score 695.5; DB 2; Length 248;

Best Local Similarity 57.8%; Pred. No. 5.1e-42;

Matches 144; Conservative 32; Mismatches 56; Indels 17; Gaps 6;

QY 23 EVOLVBSGGGVPRGSLRLSCAAGTTPDYGMWVROAPGKLEWVSGINMGSTGY 82

[illegible]

	SEQUENCE	244 AA;	26127 MW;	4B1F17868338F2BF CRC64;
QO	NON_TER	1	1	
FT	NON_TER	244	244	
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	SMART; SMO0406; IGV; 2.			
DR	SMART; SMO0409; IG; 2.			
DR	Pfam; PF00047; ig; 2.			
DR	InterPro; IPR003596; IG_v.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003599; IG.			
RL	Nat. Biotechnol. 15:629-631(1997).			
RT	"Complement recruitment using bispecific diabodies.";			
RX	Kontermann R.E., Wing M.G., Winter G.;			
RP	MEDLINE=97362799; PubMed=9219263;			
RN	[1]			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
CN	Name=scfv;			
OS	Homo sapiens (Human).			
ID	Q65ZC8	PRELIMINARY;	PRT;	244 AA.
AC	Q65ZC8;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DE	Single-chain Fv (Fragment).			

Query Match	44.2%	Score 636;	DB 2;	Length 244;
Best Local Similarity	50.8%	Pred. No. 9.1e-38;		
Matches	124;	Conservative	46;	Mismatches 64;
			Indels	10;
			Gaps	4;
Qy	23	EVQLVESGGGVYRRPGSGLRISCSAGSFPTFDIGNSWVRQAQKGIEMVSGINNGSGTGY	82	
Db	1	QVQLVQSAEAEKKPKDQSVKVSCKASGYPSFHYMYWVAQAPQGILEMGWIDPNNGDTRF	60	
Qy	83	ADSVKGRFTISRDNAKNSLYIQOMNSISRAEDPAVYYCAR-----MRAPIVIGOGGLTVYVS	136	
Db	61	AQRFGARTMTDRDISAAYMEVSLRSDRDPAAVYCAEGTGSALYGNQDWGGGLTVYS	120	
Qy	137	RGGGSGGGSGSGGGGSS-ELTODPA-VEVALGQTYRITTCQGDLSLRSYYASTYQKREGAP	194	
Db	121	SGGGSGGGSGGGGGSDIQMTQSPETLSASIGDRITTCRASGEIYHMLAWYQOKPGKAP	180	
Qy	195	VLVITYGKNNRPSGIPDRFSGSSGNTASTLTITGAQAEDEADYYCNSRDSGNHYVFGSGT	254	
Db	181	KFLITYKASLSLAGAPSRFSGSGSGTDFLTLLTSIQPDFFATYYC--QQSYNVPILTFGGGT	238	
Qy	255	KLTIV	258	
Db	239	KLEI	242	

RESULT 6	0921A6	PRELIMINARY;	PRT;	241 AA.
ID	0921A6			
CD	0921A6			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Anti-CEA 79 single chain Fv (Fragment).			
OS	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCHI_TaxID=10090;			
UN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96170165; PubMed=9509426;			
RA	Chung J.H., Choi S.-J., Kim H.-J., Kim I.-J., Choi I.H., Lee S.D.,			
RY	Yi K.S., Suh P.-G., Ryu S.H., Chung H.K.;			
RT	"Cloning and characterization of cDNAs encoding VH and VL of a			
RT	monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and			
RL	generation of a single-chain Fv molecule (scFv).";			
RL	Mol. Cells 7:816-819(1997).			
DR	EMBL; U88067; AAB48044.1; --.			
DR	PIR; S19965; S19965.			
DR	PIR; S19967; S19967.			
DR	PIR; S19968; S19968.			
DR	PIR; S26325; S26325.			
DR	HSSP; P01607; 1BMW.			
DR	SMART; SMO0406; IGV. 2.			
DR	PROSITE; PSS0835; IG_LIKE. 2.			
DR	NON_TER	1		
FT		1	241	
FT	SEQUENCE	241 AA;	26086 MW;	0276887248B5C771 CRC64;

	Query March	41.7%; Score 600; DB 2;	Length 241;
	Best Local Similarity	51.9%; Pred. No. 3.4e-35;	
	Matches 126;	Conservative 34;	Mismatches 67; Indels 16; Gaps 6;
Qy	23 EVQLVESGGGVYPRPGSGSLRLSCAASGFTFPDDYGSMWROAPGKGLENVWGGINMGSGSTGY	82	
Dd	1 QVLTQDSGPBLAKRGETIVKISCRASGTTFPDYGNMWKQAPGKLKMGMINTTYGEPTY	60	
Qy	83 ADVSKGRFTISRDNAAKNSLYLQNMNLSRAEDTAVYYCAR---	MRAPVIWGQETLVTSRGG	139
Dd	61 ADPKRGFAPSLERLESASTAYLIQINLNKNEDATYFCARLKOLLRFYDWGGTTVTYSGG	120	
Qy	140 GSGSGSGSGSGSGSS--ELTDQP-AVSVALAGOTVRITCGDLSRSTYSASWYOQKPEQAP---	194	
Dd	121 GGSFGSGSGSGSGSPSIELTGSPSSIASLGKKVITTCASODINKYIAMIQHKKPEKGRSA	180	
Qy	195 -VLVIYKGNRRPSGIPIRFGSSSGSNASLTITGAQMEDADVDYCNARDSSGNHNVRCGG	253	
Dd	181 HTLTAIYIQ---PGLPERFSGSGGRDYSPSISNLTEPEDATYATCYLAHYD---MLHTFGGG	233	
Qy	254 TKL	256	
Dd	234 TKL	236	

RESULT 7		
Q7T0M2		
ID	Q7T0M2	PRELIMINARY; PRT; 243 AA.
AC	Q7T0M2;	
DT	01-OCT-2003 (TREMBLrel. 25, Created)	
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 25, Last annotation update)	
DE	ScFv 6H8 protein (Fragment).	
GN	Name=ScFv 6H8;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI	TaxID=10090;	

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/C;
 RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
 RA Peter J.C., Efekhari P., Billfeld P., Wallukat G., Hoebeke U.;
 RT "scf single chain antibody variable fragment as inverse agonist for
 RL the beta-2 adrenergic receptor";
 RJ J. Biol. Chem. 278:36740-36747(2003).
 DR EMBL: AJ574851; CA00495.1; -;
 DR HSSP: P01751; 1A6W.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 2.
 DR PROSITE: PS50835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 243 AA; 25976 MW; BEPFE6AD2DC64F76 CRC64;

Query Match 40.1%; Score 578; DB 2; Length 243;
 Best Local Similarity 49.4%; Pred. No. 1.3e-33;
 Matches 118; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 23 EVOLVESGGGVAPGSLRLSCAASGFTPDYGMVSRAPGKGLEWVSGINNGSTGY 82
 DB 1 QVQLQSGSELPVPGASVKLSCKASGFTFTTMMHWKQHGQGLEWIGNITFGSGITNY 60
 QY 83 ADSVKRFTISRDNANKSLYLQNSLRAPEDTAVYYCAR-MRAVINGQGTLLTVSRGGGG 141
 DB 61 DEKFKKGLITVDTSSSTAVMHLSSLASEDSAVYYCARGRGLDWAGTTLTVSSGGGG 120
 QY 142 SGGGGSGGGGSS-ELTD-DPAVSVALGQTVRITTCQDSLRSYASWYQKPGQAPLVLY 199
 DB 121 SGGGGSGGGGSDIQMTQSSSPSVSLGDRVTITCKASEDIYNRLAWYQKPGAPRLLIS 180
 QY 200 GKNNRPSGIPDRSGSSSGNTASLTITGAQEDADYCNRSRSGNHVFGGTXLT 258
 DB 181 GATSLGVPSRPSGSGSKDYTLSTLTQTEDVATYTCQYWSTR--TFGGSTKLEI 236

RESULT 8

Q9NSD6 PRELIMINARY; PRT; 107 AA.

AC Q9NSD6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Homo sapiens This CDS feature is included to show the translation of
 DE the corresponding V_region. Presently translation qualifiers on
 DE V_region features are illegal. (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocyte;
 RA Hohmann A.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: LA3092; AAA69746.2; -;
 DR FTR: S70444; S70444.
 DR HSSP: P01709; 2MCG.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 38.3%; Score 552; DB 2; Length 107;
 Best Local Similarity 98.1%; Pred. No. 3.8e-32;
 Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 154 ELTDPAVSVALGQTVRITTCQDSLRSYASWYQKPGQAPLVLYGKNNRPSGIPDRFS 213

DB 1 ELTDPAVSVALGQTVRITTCQDSLRSYASWYQKPGQAPLVLYGKNNRPSGIPDRFS 60
 QY 214 GSSSGNTASLTITGAQEDADYCNRSRSGNHVFGGTXLTVLG 260
 DB 61 GSSSGNTASLTITGAQEDADYCNRSRSGNHVFGGTXLTVLG 107

RESULT 9

Q9HCC1 PRELIMINARY; PRT; 112 AA.

AC Q9HCC1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Single chain Fv (fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB049915; BAB16829.1; -;
 DR HSSP: P01783; 1IGC.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 112
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A5EC3B84788 CRC64;

Query Match 38.2%; Score 550.5; DB 2; Length 112;
 Best Local Similarity 94.6%; Pred. No. 5.2e-32;
 Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 23 EVOLVESGGGVAPGSLRLSCAASGFTPDYGMVSRAPGKGLEWVSGINNGSTGY 82
 DB 1 EVOLVESGGGVAPGSLRLSCAASGFTPDYGMVSRAPGKGLEWVSGINNGSTGY 60
 QY 83 ADSVKRFTISRDNANKSLYLQNSLRAPEDTAVYYCAR-MRAVINGQGTLLTV 133
 DB 61 ADSVKRFTISRDNANKSLYLQNSLRAPEDTAVYYCAR-RAYLDYWGQGLV 112

RESULT 10

Q65ZL2 PRELIMINARY; PRT; 487 AA.

AC Q65ZL2;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Fv/M4.
 GN Name=M4-IFN- γ -tau;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96272580; PubMed=8688499;
 RA Qi Y., Xiang J.;
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
 RT antibody secreted from myeloma cells";
 RL Hum. Antibodies Hybridomas 6:161-166(1995).
 DR EMBL: S82493; AAB37424.2; -;
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.

Best Local Similarity 92.6%; Pred. No. 2,4e-30;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 153 SELTODPAVSVALGQVTRITCOGDSLRSYVSWYQOKPGQAPVLYIGKNNRSGIPDR 212
DB 1 SELTODPAVSVALGQVTRITCOGDSLRSYVSWYQOKPGQAPVLYIGKNNRSGIPDR 60
QY 213 SGGSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGKTLTYLG 260
DB 61 SGGSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGKTLTYLG 108

RESULT 13

Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambolt R., Heidner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.,
RL Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BK40627; CAB5781.1; -
DR HSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 35.8%; Score 516; DB 2; Length 472;
Best Local Similarity 47.3%; Pred. No. 7.1e-29;
Matches 116; Conservative 20; Mismatches 77; Indels 32; Gaps 5;

QY 13 LLLAAPMAEVOVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWVROAPGKLEWVG 72
DB 10 LLLAALGVOCEVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWVROAPGKLEWVG 69
QY 73 INNNGSTGYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCAR-----MRAP 124
DB 70 ISNNSGSIAYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCAKEIGAHNFYYGM 129
QY 125 VIVGGQTLVTVSRGGGGSGGGGSSSELTODPAVSVALGQVTRITCOGDSLRSYVSW 184
DB 130 DVWGQGTITVTVS-----SASTKQPSVFPPLAPSSKSTSGGTAALGC---LVKDYFPE 177
QY 185 WYQOKPGQAPVLYIGKNNRSGI---PDRFSGSSGNTASLTITGAQAEDEADYYCNSR 241
DB 178 -----PVTYSWNSGALTSVHTFPAVLQSSGLVSSVTVTPSSSLGTOTYICNVN 228
QY 242 DSSGN 246
DB 229 HKPSN 233

RESULT 14

Q6N5K4 PRELIMINARY; PRT; 499 AA.
AC Q6N5K4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange S.J.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -
DR HSP; P01876; IOW0.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C9B9582054F32 CRC64;

Query Match 35.5%; Score 511; DB 2; Length 499;
Best Local Similarity 49.6%; Pred. No. 1.7e-28;
Matches 121; Conservative 16; Mismatches 49; Indels 58; Gaps 8;

QY 13 LLLAAPMAEVOVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWVROAPGKLEWVG 72
DB 10 LLLAALGVOCEVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWVROAPGKLEWVS 69
QY 73 INNNGSTGYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPV----- 125
DB 70 INNNGSTGYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARDPYKXCSGSSCL 129
QY 126 -----IWGGQTLVTVSRGGGGSGGGGSSSELTODPAVSVALGQVTRITCOGDSL 173
DB 130 GYMDVWGKGTITVTVS-----SASPTSPKVFPLSLCSTQPDGNNVIACTV 174
QY 174 QGSLRSYVSWYQOKP-----GQAPVLYIGKNNRSGIPDRFSGSSGNTASLTIT 225
DB 175 QG-----FPQEPFLSVTWSGQG-----VTARNFPS-----QDASGDLTYTSSQTL 218

Qy 226 TGAQ 229
Db 219 PATQ 222

RESULT 15

Q8WU38 PRELIMINARY; PRT; 573 AA.
AC 08WU38;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skaleja U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSSP; P18529; 118K.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KM Hypoetical protein.
SQ SEQUENCE 573 AA; 62967 MW; ED072344033AC530 CRC64;

Query Match 35.3%; Score 508; DB 2; Length 573;
Best Local Similarity 48.4%; Pred. No. 3.2e-28;
Matches 119; Conservative 18; Mismatches 61; Indels 48; Gaps 6;

Qy 13 LLLAQPAMAEVQLVESGGGVVPRGSLRLSCAASGFTPDYCKMHWYRQAPGKLEWVSG 72
Db 10 LLLAQLKGVCEVQLVESGGGVVPRGSLRLSCAASGFTPDYAMHWYRQAPGKLEWVSG 69
Qy 73 INNGSGTGYADSVYKGRFTISRDAKNSLYIQOMSLRAEDTAVYYCARMRAPV----- 125
Db 70 ISMWSGSIQYADSVYKGRFTISRDAKNSLYIQOMSLRAEDTALYYCAKHSGLSYGYG 129
Qy 126 --IWGCTLVTVSRGGSGGGGGGGSSSLTQDPAVSVL-----GQTVRITC-- 173

Db 130 MDVWGGTTVTV-----SSAPTKADVPFPIISGCRHPKONSPLVLAQLI 173
Qy 174 QGDSLSRYASWYQOKRGAFLVLYIKNNRP-S-GIPDRFGSSSGNTALITGAQAE 232
Db 174 TGIHPTISVTVTWI-----GTGQSFORTPEIORRDSYNTSSQLSTPLQQR 221
Qy 233 EADYYC 238
Db 222 QGEYKC 227
Search completed: April 25, 2005, 20:34:00
Job time : 145.106 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 150.818 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926d-208

Perfect score: 1303
Sequence: 1 MEVQLVESGGGVVPRPGSLR.....VVFGGTKLTVLGGGCKAK 246

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Lifting first 45 summaries

Database:

A: Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303	100.0	246	5	ABG78329 Human Fv
2	1303	100.0	246	5	ABG92026 Antibody
3	1273	97.7	256	5	ABG78334 Human Fv
4	1273	97.7	256	5	ABG92025 Antibody
5	1260.5	96.7	266	5	ABG92020 Human ant
6	1257	96.5	277	5	ABG78150 Human Fv
7	1257	96.5	277	5	ABG91841 Human ant
8	1253	96.2	277	8	AD128366 Human scf
9	1233	94.6	277	5	ABG78328 Human Fv
10	1233	94.6	277	5	ABG92019 Human ant
11	1218.5	93.5	239	5	ABP44926 Human Bly
12	1218.5	93.2	239	7	ADG95753 Single ch
13	1214.5	93.2	278	8	AD128367 Human scf
14	1212.5	93.1	239	5	ABP46027 Human Bly
15	1212.5	93.1	239	7	ADG96854 Single ch
16	1210.5	92.9	280	8	ADJ57363 P-selecti
17	1203.5	92.4	280	8	AD128368 Human scf
18	1191.5	91.4	239	5	ABP46004 Human Bly
19	1191.5	91.4	239	7	ADG96831 Single ch
20	1181	90.6	238	3	AAV95198 Anti-Plat
21	1178	90.4	244	6	AAO31136 Human CMO
22	1178	90.4	309	2	AAW83322 Single ch
23	1178	90.4	309	5	ABB09603 Amino aci
24	1178	90.4	309	6	ABG74384 Single ch
25	1178	90.4	309	7	ADG98737 Human sin

ALIGNMENTS

RESULT 1	ABG78329	standard; protein; 246 AA.
ID	ABG78329	standard; protein; 246 AA.
XX	ABG78329;	
XX	15-NOV-2002	(first entry)
DT	15-NOV-2002	(first entry)
XX	Human Fv molecule	hypervariable region related peptide #204.
XX	Human Fv molecule	hypervariable region; single chain Fv; cytostatic;
KW	disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;	
KW	lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.	
OS	Homo sapiens.	
XX	WO200259264-A2.	
PN	WO200259264-A2.	
XX	01-AUG-2002.	
PD	01-AUG-2002.	
XX	31-DEC-2001; 2001WO-US049440.	
PF	31-DEC-2001; 2001WO-US049440.	
XX	29-DEC-2000; 2000US-00751181.	
PR	29-DEC-2000; 2000US-00751181.	
XX	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
XX	Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;	
PI	Plaksin D, Peretz T;	
PI	WPI; 2002-619166/66.	
DR	Novel peptide/polypeptide for cancer therapy has Fv molecule, construct	
PT	or fragment, or construct of fragment with enhanced binding	
PT	characteristic so as to selectively bind target cell in favor of other	
XX	cells.	
PS	Disclosure; Page 44-45; 232pp; English.	
XX	The invention relates to a peptide or polypeptide comprising an Fv	Ado40446 Human sin
XX	molecule, a construct or fragments or a construct of a fragment with	Abg92023 Antibody
CC	enhanced binding characteristics which selectively and/or specifically	Ad158068 Reg IV-sp
CC	binds to a target cell in favour of other cells, where binding is	Abg92024 Antibody
CC	primarily determined by a first hypervariable region and Fv is a single	Abp46007 Human Bly
CC	chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in	Abp46007 Human Bly
CC	association with or attached, coupled, linked or fused to a	AAO31139 Human CMO
CC	pharmaceutical agent, is useful in the manufacture of a medicament, where	Abp46024 Human Bly
CC	the medicament has activity against a diseased cell, preferably a cancer	Adg96851 Single ch
CC	cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,	AAO31137 Human CMO
CC		Adp45405 Human Bly
CC		Adg96232 Single ch
CC		Adg96232 Single ch
CC		Abp46045 Human Bly
CC		Adg96872 Single ch
CC		Abp46012 Human Bly
CC		Adg96839 Single ch
CC		Adg30497 Human GMC
CC		Abp46002 Human Bly
CC		Adg96829 Single ch

CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
CC acute myeloid leukemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 1303; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVOLVESGGGAVRPGSGSLRLSCAAGFTFDDYGMGSMVWRQAPKGLGEMVSGINMNGSGSTG 60
DB 1 MEVOLVESGGGAVRPGSGSLRLSCAAGFTFDDYGMGSMVWRQAPKGLGEMVSGINMNGSGSTG 60
QY 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMRAPVWGQGLTVTSRGGGG 120
DB 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMRAPVWGQGLTVTSRGGGG 120
QY 121 SGGGSGGGGSSSLTODPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYK 180
DB 121 SGGGSGGGGSSSLTODPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYK 180
QY 181 NNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGTRKLTVLGG 240
DB 181 NNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGTRKLTVLGG 240
QY 241 GGCKAK 246
DB 241 GGCKAK 246

RESULT 2
ABG92026
ID ABG92026 standard; protein; 246 AA.

XX ABG92026;
XX
DT 04-DEC-2002 (first entry)
XX
XX Antibody protein #5.
XX
XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX metastasis; hypervariable region; autoimmune disease; thrombosis;
XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX myocardial infarction; retinopathic disease; abnormal platelet function;
XX sulphated tyrosine-dependent protein-protein interaction.
XX
XX Unidentified.
XX
XX
XX WO200253700-A2.
XX
XX 11-JUL-2002.
XX
XX 31-DEC-2001; 2001WO-US049442.
XX
XX 29-DEC-2000; 2000US-00751181.
XX
XX 29-DEC-2000; 2000US-0258948P.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX Lazarevits J, Hagai Y, Plaksein D, Vogel T, Nimrod A, Mar-Haim H;
XX Sanchon E, Richter T, Amit B, Kooperman L, Feretz T, Levanon A;
XX
XX WPI; 2002-674776/72.
XX
XX
XX Novel isolated epitope present on cancer cells and important in
XX physiological phenomena such as cell rolling, metastasis and
XX inflammation, for treating autoimmune, inflammatory or cardiovascular
XX diseases, and cancer.
XX
XX Disclosure; Fig 52; Opp; English.

XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukemia cells, increase in number of tumour or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumour or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune disease, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents an antibody protein of the
CC invention
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 1303; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVOLVESGGGAVRPGSGSLRLSCAAGFTFDDYGMGSMVWRQAPKGLGEMVSGINMNGSGSTG 60
DB 1 MEVOLVESGGGAVRPGSGSLRLSCAAGFTFDDYGMGSMVWRQAPKGLGEMVSGINMNGSGSTG 60
QY 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMRAPVWGQGLTVTSRGGGG 120
DB 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMRAPVWGQGLTVTSRGGGG 120
QY 121 SGGGSGGGGSSSLTODPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYK 180
DB 121 SGGGSGGGGSSSLTODPAVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYYK 180
QY 181 NNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGTRKLTVLGG 240
DB 181 NNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGTRKLTVLGG 240
QY 241 GGCKAK 246
DB 241 GGCKAK 246

RESULT 3
ABG78334
ID ABG78334 standard; protein; 256 AA.

XX ABG78334;
XX
DT 15-NOV-2002 (first entry)
XX
XX Human Fv molecule hypervariable region related peptide #209.
XX
XX
XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukemia; adenoma;
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.
XX
XX Homo sapiens.
XX
XX
XX WO200259264-A2.
XX
XX 01-AUG-2002.
XX
XX 31-DEC-2001; 2001WO-US049440.
XX
XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
PI Plakain D, Peretz T;
XX WPI; 2002-619166/66.
DR
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Example 9; Page 90; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct and/or specifically
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 256 AA;
Query Match 97.7%; Score 1273; DB 5; Length 256;
Best Local Similarity 99.6%; Pred. No. 1.9e-80;
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVVRQAPGKLEWVGIMNGSGTG 60
DB 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVVRQAPGKLEWVGIMNGSGTG 60
QY 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMAPYIWQGTLVTVSRGGG 120
DB 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMAPYIWQGTLVTVSRGGG 120
QY 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGQAPLVLYYK 180
DB 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGQAPLVLYYK 180
QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240
DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240
QY 241 GG 242
DB 241 GG 242
RESULT 4
ID ABG92025 standard; protein; 256 AA.
XX ABG92025;
AC 04-DEC-2002 (first entry)
XX Antibody biotag #1.
XX Antibody biotag #1.
XX Antibody, antibody biotag; cancer; tumour; cell rolling; inflammation;
KM metastasis; hypervariable region; autoimmune disease; thrombosis;
KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KM myocardial infarction; retinopathic disease; abnormal platelet function;
KM sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.
OS
XX NO200253700-A2.
PN
XX 11-JUL-2002.
PD
XX 31-DEC-2001; 2001WO-US049442.
PF
XX 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
PA Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
PI Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI; 2002-674776/72.
DR
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
XX Disclosure; Fig 51; Opp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents an antibody biotag used in
CC the scope of the invention
XX
SQ Sequence 256 AA;
Query Match 97.7%; Score 1273; DB 5; Length 256;
Best Local Similarity 99.6%; Pred. No. 1.9e-80;
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVVRQAPGKLEWVGIMNGSGTG 60
DB 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVVRQAPGKLEWVGIMNGSGTG 60
QY 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMAPYIWQGTLVTVSRGGG 120
DB 61 YADSVKGRFTISRDNAKNSLYLQMNSLRADTVAVYCARMAPYIWQGTLVTVSRGGG 120
QY 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGQAPLVLYYK 180
DB 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGQAPLVLYYK 180
QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240
DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240
QY 241 GG 242
DB 241 GG 242

RESULT 5
 ABG92020 standard; protein; 266 AA.
 ID ABG92020 standard; protein; 266 AA.
 AC ABG92020;
 XX
 DT 04-DEC-2002 (first entry)
 DE Human antibody fragment #204.
 XX
 KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.

Novel isolated epitope present on cancer cells and important in
 physiological phenomena such as cell rolling, metastasis and
 inflammation, for treating autoimmune, inflammatory or cardiovascular
 diseases, and cancer.

Disclosure; Page 309-310; Opp; English.

The invention relates to an isolated epitope present on cancer cells and
 important in physiological phenomena such as cell rolling, metastasis and
 inflammation, where the epitope is capable of being bound by an antibody,
 its antigen-binding fragment or its complex comprising at least one
 antibody or its binding fragment having a first hypervariable region. The
 epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 disease, thrombosis, restenosis, metastasis, growth and/or replication of
 tumour or leukaemia cells, increase in number of tumour or leukaemia
 cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 platelet and/or cell-platelet adhesion or aggregation, for increasing
 mortality of tumour or leukaemia cells, for increasing the susceptibility
 of diseased cells to damage by anti-disease, anti-cancer or anti-
 leukaemia agents, or for decreasing the number of tumour or leukaemia
 cells in a patient, or in the manufacture of a medicament for the above
 mentioned purposes. The epitopes are useful for diagnosing and treating
 diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 diseases, cardiovascular diseases such as myocardial infarction,
 retinopathic diseases and other diseases mediated by abnormal platelet
 function and diseases caused by sulphated tyrosine-dependent protein-
 protein interactions. This sequence represents a human antibody fragment
 of the invention

Sequence 266 AA;

Query Match 96.7%; Score 1260.5; DB 5; Length 266;

Best Local Similarity 98.4%; Pred. No. 1.4e-79;

Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

2 EVOLVESGGGVPRPGSGSLRLSCAASGFTFDYGMGHWROAPGKLEWVSGINMGSGTGY 61

|||||

DB 23 EVOLVESGGGVPRPGSGSLRLSCAASGFTFDYGMGHWROAPGKLEWVSGINMGSGTGY 82
 QY 62 ADSVKGRFTISRDNAKNSLYLQNMSLRADTAVYVCARFARAVIWQGTLYTVSRGGGS 121
 DB 83 ADSVKGRFTISRDNAKNSLYLQNMSLRADTAVYVCARFARAVIWQGTLYTVSRGGGS 142
 QY 122 GGGSGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWYQKPGQAPLVLYGN 181
 DB 143 GGGSGGGSSSELTPDPAVSVALGQTVRTTCGDSLRSYASWYQKPGQAPLVLYGN 202
 QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQADEADYYNCSRDSSGNHVPFGGTRKLYLGGS 241
 DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQADEADYYNCSRDSSGNHVPFGGTRKLYLV-CA 261
 QY 242 GCKAK 246
 DB 262 AAKAK 266

RESULT 6
 ABG78150 standard; protein; 277 AA.
 ID ABG78150 standard; protein; 277 AA.
 AC ABG78150;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #25.

Human Fv molecule hypervariable region related peptide #25.

Human; Fv molecule; hypervariable region; single chain Fv; cyrostatic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX
 DR WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

Claim 4; Page 155-156; 232pp; English.

The invention relates to a peptide or polypeptide comprising an Fv
 molecule, a construct or fragments or a construct of a fragment with
 enhanced binding characteristics which selectively and/or specifically
 binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has actively against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 related peptide of the invention

SQ Sequence 277 AA;
 Query Match 96.5%; Score 1257; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-79;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVOLVESGGGVVAPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINNGSGTGY 61
 DB 23 EVOLVESGGGVVAPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINNGSGTGY 82
 QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRADDTAVYYCARMAPYIWGGTLVTVSRGGGS 121
 DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRADDTAVYYCARMAPYIWGGTLVTVSRGGGS 142
 QY 122 GGGSGGGGSELTOPDAVVALGQVTRITCOGDSLRSYASWYQOKRQGA PVLVIYGN 181
 DB 143 GGGSGGGGSELTOPDAVVALGQVTRITCOGDSLRSYASWYQOKRQGA PVLVIYGN 202
 QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGGTKLTVLG 239
 DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGGTKLTVLG 260

RESULT 7
 ABG91841
 ID ABG91841 standard; protein; 277 AA.
 AC ABG91841;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #25.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN MO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001MO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Claim 23; Page 233-234; Opp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

SQ Sequence 277 AA;
 Query Match 96.5%; Score 1257; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-79;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVOLVESGGGVVAPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINNGSGTGY 61
 DB 23 EVOLVESGGGVVAPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINNGSGTGY 82
 QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRADDTAVYYCARMAPYIWGGTLVTVSRGGGS 121
 DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRADDTAVYYCARMAPYIWGGTLVTVSRGGGS 142
 QY 122 GGGSGGGGSELTOPDAVVALGQVTRITCOGDSLRSYASWYQOKRQGA PVLVIYGN 181
 DB 143 GGGSGGGGSELTOPDAVVALGQVTRITCOGDSLRSYASWYQOKRQGA PVLVIYGN 202
 QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGGTKLTVLG 239
 DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGGTKLTVLG 260

RESULT 8
 ADI28366
 ID ADI28366 standard; protein; 277 AA.
 AC ADI28366;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment Y1, binds to platelets.
 XX
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO2004002528-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003MO-US020604.
 XX
 PR 01-JUL-2002; 2002US-00189025.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 DR WPI; 2004-099189/10.
 XX
 CC Composition comprising an agent and/or antibody or its fragment, useful
 CC for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 CC for inhibiting growth and/or replication of tumor cells or leukaemia
 CC cells.
 XX
 PS Claim 13; SEQ ID NO 1; 58pp; English.
 XX
 CC The present sequence is the protein sequence of human scFv fragment Y1.
 CC This antibody was identified by screening a human antibody phage library

CC that has diversity only in the heavy chain CDR3 regions. Fixed human
CC platelets were screened in order to identify antibodies that bind
CC platelets. The epitope for Y1 antibody is located between amino acids 272
CC and 285 on glycoprotein, a subunit of the CD2 complex. Y1 also binds the
CC N-terminal of PEG-1, a receptor for E-, L- and P-selectins, and has a
CC high affinity for primary leukaemia cells. The invention relates to
CC compositions utilising an agent and an antibody or its fragment. The
CC agent is a toxin, radioisotope or pharmaceutical agent such as
CC doxorubicin. It is complexed or combined with or conjugated to the
CC antibody or its fragment. The agent and/or antibody can be present in the
CC composition as a sub-clinical amount, i.e. less than the amount generally
CC found to be clinically effective when the agent is administered alone.
CC The composition is used in claimed methods of: inhibiting cell rolling,
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC replication of tumour cells or leukaemia cells, an increase in number of
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet complex formation, aggregation or
CC adhesion; increasing the mortality rate of tumour or leukaemia cells; the
CC susceptibility of disease cells to damage by anti-disease agents, and the
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
CC agents; and ameliorating the effects of a disease, preventing a disease,
CC treating a disease or inhibiting the progress of a disease.

XX
XX
SQ Sequence 277 AA:

Query Match 96.2%; Score 1253; DB 8; Length 277;
Best Local Similarity 99.6%; Pred. No. 4.9e-79;
Matches 23/; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVOLVSSGGGVVPPGSLRLSCAASGFTPDYGMVWVRAQPGKLEWVSGINNNGSTGY 61
DB 23 EVOLVSSGGGVVPPGSLRLSCAASGFTPDYGMVWVRAQPGKLEWVSGINNNGSTGY 82
QY 62 ADSVKGRTTISRDNAAKSLYLQNSLRADTAIVYCCARMAPYIWGGTLVTVSRGGGS 121
DB 83 ADSVKGRTTISRDNAAKSLYLQNSLRADTAIVYCCARMAPYIWGGTLVTVSRGGGS 142
QY 122 GGGSGGGGSSSELTQDPAVSVVALGQTVRITCGDSLSRSYASVYQKPGQAPVLYVYGN 181
DB 143 GGGSGGGGSSSELTQDPAVSVVALGQTVRITCGDSLSRSYASVYQKPGQAPVLYVYGN 202
QY 182 NRPSGIPDRPSSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTYLTVLG 239
DB 203 NRPSGIPDRPSSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTYLTVLG 260

RESULT 9
ABG78328
ID ABG78328 standard; protein; 277 AA.
XX
XX ABG78328;

XX
XX 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #203.

XX
XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;
KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
XX Homo sapiens.

OS
XX
PN NO200259264-A2.

XX
XX 01-AUG-2002.

XX
XX 31-DEC-2001; 2001WO-US049440.

XX
XX 29-DEC-2000; 2000US-00751181.

XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PA Hagai Y, Lazarovits J, Guy R, Lipchitz O, Szanton E, Levanon A;
PI

PI Plakain D, Peretz T;
XX
XX MPI: 2002-619166/66.
DR N-PSDB; ABS63384.

XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.

XX
XX Claim 141; Fig 14; 222pp; English.

XX
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention

XX
XX SQ Sequence 277 AA:

Query Match 94.6%; Score 1233; DB 5; Length 277;
Best Local Similarity 97.9%; Pred. No. 1.2e-77;
Matches 23/; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EVOLVSSGGGVVPPGSLRLSCAASGFTPDYGMVWVRAQPGKLEWVSGINNNGSTGY 61
DB 23 EVOLVSSGGGVVPPGSLRLSCAASGFTPDYGMVWVRAQPGKLEWVSGINNNGSTGY 82
QY 62 ADSVKGRTTISRDNAAKSLYLQNSLRADTAIVYCCARMAPYIWGGTLVTVSRGGGS 121
DB 83 ADSVKGRTTISRDNAAKSLYLQNSLRADTAIVYCCARMAPYIWGGTLVTVSRGGGS 142
QY 122 GGGSGGGGSSSELTQDPAVSVVALGQTVRITCGDSLSRSYASVYQKPGQAPVLYVYGN 181
DB 143 GGGSGGGGSSSELTQDPAVSVVALGQTVRITCGDSLSRSYASVYQKPGQAPVLYVYGN 202
QY 182 NRPSGIPDRPSSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTYLTVLG 239
DB 203 NRPSGIPDRPSSGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTYLTVLG 260

RESULT 10
ABG92019
ID ABG92019 standard; protein; 277 AA.
XX
XX ABG92019;

XX
XX 04-DEC-2002 (first entry)

DE Human antibody fragment #203.

XX
XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KM myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.

XX
XX Homo sapiens.

OS
XX
PN NO200253700-A2.

XX
XX 11-JUL-2002.

XX
XX

PF	31-DEC-2001; 2001WO-US049442.
PR	29-DEC-2000; 2000US-00751181.
PR	29-DEC-2000; 2000US-0258948P.
XX	
XX	
XX	(BIOT-) BIO-TECHNOLOGY GEN CORP.
PA	Lazarovite J, Hengal Y, Plakkein D, Vogel T, Nimrod A, Mar-Haim H;
PI	Szathon E, Richter T, Amlt B, Kooperman L, Peretz T, Levanon A;
XX	WP1; 2002-674776/72.
XX	
PT	Novel isolated epitope present on cancer cells and important in
PT	physiological phenomena such as cell rolling, metastasis and
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular
PT	diseases, and cancer.
XX	
PS	Claim 23; Page 308-309; Opp; English.
CC	The invention relates to an isolated epitope present on cancer cells and
CC	important in physiological phenomena such as cell rolling, metastasis and
CC	inflammation, where the epitope is capable of being bound by an antibody,
CC	its antigen-binding fragment or its complex comprising at least one
CC	antibody or its binding fragment having a first hypervariable region. The
CC	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC	disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC	tumour or leukaemia cells, increase in number of tumour or leukaemia
CC	cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC	platelet and/or cell-platelet adhesion or aggregation, for increasing
CC	mortality of tumour or leukaemia cells, for increasing the susceptibility
CC	of diseased cells to damage by anti-disease, anti-cancer or anti-
CC	leukaemia agents, or for decreasing the number of tumour or leukaemia
CC	cells in a patient, or in the manufacture of a medicament for the above
CC	mentioned purposes. The epitopes are useful for diagnosing and treating
CC	diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC	diseases, cardiovascular diseases such as myocardial infarction,
CC	retinopathic diseases and other diseases mediated by abnormal platelet
CC	function and diseases caused by sulphated tyrosine-dependent protein-
CC	protein interactions. This sequence represents a human antibody fragment
CC	of the invention
XX	
XX	
XX	
SQ	Sequence 277 AA;
Query Match	94.6%; Score 1233; DB 5; Length 277;
Best Local Similarity	97.9%; Pred. NO. 1.2e-77;
Matches 233; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
QY	2 EVLVESGGGVRRPGSGIRLSCASGFFPDYGMNSWFOAPQKGLKEMVSGINWNGSGTGY 61
DB	23 EVLVESGGGVRRPGSGIRLSCASGFFPDYGMNSWFOAPQKGLKEMVSGINWNGSGTGY 82
QY	62 ADVYKGRITISRDNAKNSLYIQOMNSILRAEDPAVVYCAMBRAPVIMGOGTILTVNSRGGGGS 121
DB	83 ADVYKGRITISRDNAKNSLYIQOMNSILRAEDPAVVYCAALTHFYGGGLTVLVSNGGGGS 142
QY	122 GGGSGGGGSSSELTDDPAVSVALGQTVVITTCGDSLRSRYASWYQKRGQAPVLVIYKKN 181
DB	143 GGGSGGGGSSSELTDDPAVSVALGQTVVITTCGDSLRSRYASWYQKRGQAPVLVIYKKN 202
QY	182 NRPESGIPRRFSGSSSGNTASLTITGAQADEADYICNSRDSGSHVVFGGGTKLTVLG 239
DB	203 NRPESGIPRRFSGSSSGNTASLTITGAQADEADYICNSRDSGSHVVFGGGTKLTVLG 260
RESULT 11	
ID	ABP44926 standard; protein; 239 AA.
XX	ABP44926;
AC	
DT	19-AUG-2002 (first entry)
XX	
DE	Human Blys binding scFv SEQ ID 937.

XX	Blvs; B lymphocyte stimulator; TNF superfamily; human; cytosolic;	
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;	
KM	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;	
KM	antiaids; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;	
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200202641-A1.	
XX		
PD	10-JAN-2002.	
XX		
PF	15-JUN-2001; 2001WO-US019110.	
XX		
PR	16-JUN-2000; 2000US-0212210P.	
PR	17-OCT-2000; 2000US-0240816P.	
PR	16-MAR-2001; 2001US-0276248P.	
PR	21-MAR-2001; 2001US-0277379P.	
XX		
PR	25-MAY-2001; 2001US-0293499P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
XX		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;	
XX		
DR	WPI; 2002-114799/15.	
XX		
PT	Antibodies against B lymphocyte stimulating polypeptides, useful for the	
PT	diagnosis and treatment of cancers and immune disorders.	
XX		
PS	Claim 1; Page 1520-1521; 3148pp; English.	
XX		
CC	This invention describes novel antibodies that immunospecifically bind to	
CC	B lymphocyte stimulator (Blvs) polypeptides. Blvs is a member of the	
CC	tumour necrosis factor (TNF) super family and induces B cell	
CC	proliferation and differentiation. The antibodies of the invention have	
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,	
CC	antirheumatic and antiaids activity and can be used in vaccines to	
CC	inhibit the expression and activity of Blvs. The antibodies bind to Blvs	
CC	and so may be used to detect and quantitate the presence of Blvs in	
CC	biological samples and may be used in this way to diagnose disease	
CC	associated with aberrant expression of Blvs. They may also be	
CC	administered to treat diseases associated with aberrant Blvs expression	
CC	and actively such as cancer, immune, and autoimmune disorders and	
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,	
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and	
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent	
CC	the antibodies and fragments of the antibodies described in the method of	
XX	the invention	
XX		
S0	Sequence 239 AA:	
QY	Query Match	93.5%; Score 1218.5; DB 5; Length 239;
	Best Local Similarity	97.9%; Pred. No. 1e-76;
	Matches 234; Conservative	0; Mismatches 4; Indels 1; Gaps 1
Db	1	EVOLVESSGGIVRRRGSSRLRLSCASGFFPDYGSWVRQAPKGLGEMVSGITWNGSGTGY 61
QY	62	ADVYKGRFTISRDNKNSLYLQNMSSLRADPTAVVYCCAMR-APVIMGOOTLVTVSRGGGG 120
Db	61	ADVYKGRFTISRDNKNSLYLQNMSSLRADPTAVVYCCARRRLADYWGOGTLTVSRGGGG 120
QY	121	SGGGSGGGGSSSELTOPDAVSVALGQTVRITCOGDBSLRSYYASWYQKRGQAPVLYVYK 180
Db	121	SGGGSGGGGSSSELTOPDAVSVALGQTVRITCOGDBSLRSYYASWYQKRGQAPVLYVYK 180
QY	181	NNRPSGIPDRFGSSSGNTATLTTGAQAEADYVYCNRSRBSGNNVYFGGCTKLTVLG 239
Db	181	NNRPSGIPDRFGSSSGNTATLTTGAQAEADYVYCNRSRBSGNNVYFGGCTKLTVLG 239

RESULT 12
ADG95753
ID ADG95753 standard; protein; 239 AA.
XX
AC ADG95753;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SeqID 937.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN MO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002MO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 937; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 239 AA;
XX
Query Match 93.5%; Score 1218.5; DB 7; Length 239;
Best Local Similarity 97.9%; Pred. No. 1e-76;
Matches 233; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
XX
QY 2 EVOLVESGGGVVRRPGSGSLRLSCAASGFTPDYGMKSWRQAPGKGLVWGSGINMGSGSTGY 61
DB 1 EVOLVESGGGVVRRPGSGSLRLSCAASGFTPDYGMKSWRQAPGKGLVWGSGINMGSGSTGY 60

QY 62 ADSVKGRFTISRDNANSLYLQNNSLRAEDTAVVYCARNR-APVIWGQGLTVTSRGGG 120
DB 61 ADSVKGRFTISRDNANSLYLQNNSLRAEDTAVVYCARNRALDYGGQGLTVTSRGGG 120
QY 121 SGGGSGSGGSGSGLTDDPAVSVALGQTVRITTCQGSLSRYSVSWYQKRGQAPVLYYXK 180
DB 121 SGGGSGSGGSGSSELTDDPAVSVALGQTVRITTCQGSLSRYSVSWYQKRGQAPVLYYXK 180
QY 181 NNRPSTGTPRFGSGSSGNTASLTITGAQAEADAVYCNRSRDSGNHVFGGFKLTVLG 239
DB 181 NNRPSTGTPRFGSGSSGNTASLTITGAQAEADAVYCNRSRDSGNHVFGGFKLTVLG 239
RESULT 13
AD128367
ID AD128367 standard; protein; 278 AA.
XX
AC AD128367;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human scFv fragment Y17, binds to platelets.
XX
KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX
OS Homo sapiens.
XX
PN WO2004002528-A1.
XX
PD 08-JAN-2004.
XX
PF 30-JUN-2003; 2003MO-US020604.
XX
PR 01-JUL-2002; 2002US-00189025.
XX
PA (SAVI-) SAVIENT PHARM INC.
XX
PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX
DR WPI; 2004-099189/10.
XX
PT Composition comprising an agent and/or antibody or its fragment, useful
PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
PT for inhibiting growth and/or replication of tumor cells or leukemia
PT cells.
XX
PS Claim 13; SEQ ID NO 2; 58pp; English.
XX
CC The present sequence is the protein sequence of human scFv fragment Y17.
CC This antibody was identified by screening a human antibody phage library
CC that has diversity only in the heavy chain CDR3 regions. Fixed human
CC platelets were screened in order to identify antibodies that bind
CC platelets. Y17 binds leukemic cells. The invention relates to
CC compositions utilising an agent and an antibody or its fragment. The
CC agent is a toxin, radioisotope or pharmaceutical agent such as
CC doxorubicin. It is complexed or combined with or conjugated to the
CC antibody or its fragment. The agent and/or antibody can be present in the
CC composition is a sub-clinical amount, i.e. less than the amount generally
CC found to be clinically effective when the agent is administered alone.
CC The composition is used in claimed methods of: inhibiting cell rolling,
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC replication of tumor cells or leukaemia cells, an increase in number of
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet complex formation, aggregation or
CC adhesion; increasing the mortality rate of tumour or leukaemia cells; the
CC susceptibility of disease cells to damage by anti-disease genes; and the
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
CC agents; and ameliorating the effects of a disease, preventing a disease,
CC treating a disease or inhibiting the progress of a disease.
XX
SQ Sequence 278 AA;
XX

Query Match 93.2%; Score 1214.5; DB 8; Length 278;
 Best Local Similarity 97.5%; Pred. No. 2.3e-76;
 Matches 233; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNPPGSLRLSCAASGFTPD-DYGMKWTROAPGKLEWVGIMNNGSTG 60
 |||||
 DB 23 EVOLVESGGGVNPPGSLRLSCAASGFTPDLTHTPEFVNRQAPGKLEWVGIMNNGSTG 82
 |||||

QY 61 YADSVYGRFTISRDNKNSLYLQMNSLRAEDTAVYVCARRARAVIWGQGLTVVSRGGG 120
 |||||
 DB 83 YADSVYGRFTISRDNKNSLYLQMNSLRAEDTAVYVCARRARAVIWGQGLTVVSRGGG 142
 |||||

QY 121 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 180
 |||||
 DB 143 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 202
 |||||

QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYVCNSRDSSGNHVFPGGTRKLTVLG 239
 |||||
 DB 203 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYVCNSRDSSGNHVFPGGTRKLTVLG 261
 |||||

RESULT 14
 ABP46027
 ID ABP46027 standard; protein; 239 AA.
 XX
 AC ABP46027;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 2038.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002;
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0272379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1, Page 2830-2831; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 239 AA;

Query Match 93.1%; Score 1212.5; DB 5; Length 239;
 Best Local Similarity 97.5%; Pred. No. 2.7e-76;
 Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNPPGSLRLSCAASGFTPDYGMKWTROAPGKLEWVGIMNNGSTG 61
 |||||
 DB 1 EVOLVESGGGVNPPGSLRLSCAASGFTPDYGMKWTROAPGKLEWVGIMNNGSTG 60
 |||||

QY 62 ADSVYGRFTISRDNKNSLYLQMNSLRAEDTAVYVCARRARAVIWGQGLTVVSRGGG 120
 |||||
 DB 61 ADSVYGRFTISRDNKNSLYLQMNSLRAEDTAVYVCARRARAVIWGQGLTVVSRGGG 120
 |||||

QY 121 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 180
 |||||
 DB 121 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 180
 |||||

QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYVCNSRDSSGNHVFPGGTRKLTVLG 239
 |||||
 DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYVCNSRDSSGNHVFPGGTRKLTVLG 239
 |||||

RESULT 15
 ADG96854
 ID ADG96854 standard; protein; 239 AA.
 XX
 AC ADG96854;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds BlyS SeqID 2038.
 XX
 KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
 KW carcinoma; lymphoma; antineumatic; antichronic; neuroprotective;
 KW antiinflammatory; antiaesthetic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 DR WPI; 2003-505350/47.
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 2038; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.

XX
SQ Sequence 239 AA:

Query Match 93.1%; Score 1212.5; DB 7; Length 239;
Best Local Similarity 97.5%; Pred. No. 2.7e-76;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVAPCGSLRLSCAASGFTPDYGMWVROAPGKGLEWVSGINMGSTGY 61
DB 1 EVOLVESGGGVAPCGSLRLSCAASGFTPDYGMWVROAPGKGLEWVSGINMGSTGY 60
QY 62 ADSVKGRFTISRDNKNSLYLQMNLSLAEDTAVYYCARMR-APYIWGQGLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNKNSLYLQMNLSLAEDTAVYYCARRRYALDYWGQGLVTVSSGGG 120
QY 121 SGGGSGGGGSSSLTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPLVLYYK 180
DB 121 SGGGSGGGGSSSLTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPLVLYYK 180
QY 181 NNRPSCGIPDRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGGLTAVLG 239
DB 181 NNRPSCGIPDRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGGLTAVLG 239

Search completed: April 25, 2005, 20:22:30
Job time : 151.818 secs


```
Db 100 ADVSKRVTISRDNAKNSLYLQNNSLRAEDTAVYYCAKILGAGRGWYFDLMGKGTIVTVS 159
Qy 116 RGGGSGGGGGGGGGSSSELTODPAVSVALGQTVRITTCQDLSLSYASWYQKPGQAPVL 175
Db 160 SGGGGGGGGGGGGSSSELTODPAVSVALGQTVRITTCQDLSLSYASWYQKPGQAPVL 219
Qy 176 VIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTUL 235
Db 220 VIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTUL 279
Qy 236 TVLG 239
Db 280 TVLG 283

RESULT 2
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chundharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-10

Query Match 84.3%; Score 1098.5; DB 3; Length 312;
Best Local Similarity 87.0%; Pred. No. 6,4e-81;
Matches 214; Conservative 5; Mismatches 18; Indels 9; Gaps 1;
```

```
Qy 174 VIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGCT 233
Db 221 VIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGCT 280
Qy 234 KLTVLG 239
Db 281 KLTVLG 286

RESULT 3
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scFv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
; US-09-260-527-1

Query Match 84.1%; Score 1095.5; DB 3; Length 280;
Best Local Similarity 88.4%; Pred. No. 9,9e-81;
Matches 213; Conservative 10; Mismatches 15; Indels 3; Gaps 2;
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Qy 2 EVOLVESGGGVAPRGSLRLSCAASGFTPDYGMWVQAQPKGLEWVSGI--NNNGSGT 59
Db 23 EVOLVESGGGVAPRGSLRLSCAASGFTPSNMMWVQAQPKGLEWVGRIRKTDGGT 82
Qy 60 GYADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCAR-MRAPYIWGGTILVTVSRGG 118
Db 83 DYAPAVKGRFTISRDNKNSLYLQNNSLKTEDTAVYYCAR-KMRKALRMGGTLVTVSRGG 142
Qy 119 GSGGGGGGGGGSSSELTODPAVSVALGQTVRITTCQDLSLSYASWYQKPGQAPVLVY 178
Db 143 GSGGGGGGGGGSSSELTODPAVSVALGQTVRITTCQDLSLSYASWYQKPGQAPVLVY 202
Qy 179 GKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTUL 238
Db 203 GKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTUL 262
Qy 239 G 239
Db 263 G 263

RESULT 4
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
```



```
/ GENERAL INFORMATION:
/ APPLICANT: Kwak, Larry
/ APPLICANT: Birsayn, Arya
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
/ FILE REFERENCE: 14014.0316/P
/ CURRENT APPLICATION NUMBER: US/09/646.028
/ CURRENT FILING DATE: 2000-09-12
/ PRIOR APPLICATION NUMBER: 60/077,745
/ PRIOR FILING DATE: 1998-03-12
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FaSeq for Windows Version 3.0
/ SEQ ID NO 51
/ LENGTH: 348
/ TYPE: PRN
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

Query Match          60.9%; Score 793.5; DB 4; Length 348;
Best Local Similarity 63.9%; Pred. No. 2.7e-56;
Matches 159; Conservative 27; Mismatches 52; Indels 11; Gaps 4;

QY 1 MEVLVESGGGVVPPGSLRLSCAASGFTPDYGMVWROAPGKLEWVGGINNGSGTG 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 93 LEVQLVESGGGLVPGSSLRSLSCVSAISLTSSSAITVTRQAPGKLEWVGISFGSTTY 152
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YADSVKGRFTISRDNKNSLYLQNSIRAEEDTAVYICARRAPVI---WGQTLVTV-S 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 153 YADSVKGRFASRSDNSKNTVYLQNNLRPNMTAVYFCANNQTFCLDNWGQGLTVTVSS 212
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 RGGGSGGGGGGGGGG---SELTPDPAVSVALGQTVRITQGSLSR---SYASWYQKP 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 213 RGGGSGGGGGGGGGGSGSVLTQPPSVSAAPGQRTVISTGSRSNIGAGYDVNWYQKFP 272
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 170 GQAPVLYIVGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVP 229
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 273 ETAPKVLIVYNNRPFSGVPDRFSGSKSGTASLAIITQLQEDGTYTCQCNDSLSGMLF 332
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 230 GGGTKLTVL 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 333 GGGTKLTVL 341

RESULT 11
US-08-918-148-75
/ Sequence 75, Application US/08918148A
/ Patent No. 6342220
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camellia
/ APPLICANT: W.
/ APPLICANT: Carter, Paul J.
/ APPLICANT: Fendly, Brian M.
/ APPLICANT: Gurney, Austin L.
/ TITLE OF INVENTION: Agonist Antibodies
/ FILE REFERENCE: P0979
/ CURRENT APPLICATION NUMBER: US/08/918.148A
/ CURRENT FILING DATE: 1997-08-25
/ NUMBER OF SEQ ID NOS: 79
/ SEQ ID NO 75
/ LENGTH: 245
/ TYPE: PRN
/ ORGANISM: artificial
US-08-918-148-75

Query Match          59.4%; Score 774.5; DB 3; Length 245;
Best Local Similarity 65.1%; Pred. No. 6.1e-55;
Matches 157; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

QY 2 EVQLVSGGGVVRPGSLRLSCAASGFTPDYGMVWROAPGKLEWVGGINNGSGTGY 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 EVQLVSGGGGLVPPGSLRLSCAASGFTPDYGMVWROAPGKLEWVGISFGSTTY 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 230 GGGTKLTVL 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 333 GGGTKLTVL 341
```

```
QY 62 ADSVKGRFTISRDNKNSLYLQNSIRAEEDTAVYICARRM---APVIWGQTLTVTSRGG 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 ADSVKGRFTISRDNKNSLYLQNSIRAEEDTAVYICARRMGEADAFDIWGQTVTVSSGG 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 GSGGGGGGGGGSS-ELTPDPA-VSVALGQTVRITQGSLSRYSWYQKPPQAPVLV 176
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 GSGGGGGGGGGSDIVWTQSPSTLSASVGDRAVITCRASBGIVHMLAWYQKPKAPKL 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPVGGT 236
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 183 IYKASSLSAGAPRFRFSGSGADFTLITSLQPDDEATYYC---QQYSNYPVLTGGG 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 237 V 237
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 V 241

RESULT 12
US-09-138-091A-73
/ Sequence 73, Application US/09138091A
/ Patent No. 6737249
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camellia W.
/ APPLICANT: Carter, Paul J.
/ APPLICANT: Fendly, Brian M.
/ APPLICANT: Gurney, Austin L.
/ TITLE OF INVENTION: Agonist Antibodies
/ FILE REFERENCE: 9491-013-27
/ CURRENT APPLICATION NUMBER: US/09/138.091A
/ CURRENT FILING DATE: 1998-08-21
/ PRIOR APPLICATION NUMBER: US 60/056,736
/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FaSeq for Windows Version 4.0
/ SEQ ID NO 73
/ LENGTH: 245
/ TYPE: PRN
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73

Query Match          59.4%; Score 774.5; DB 4; Length 245;
Best Local Similarity 65.1%; Pred. No. 6.1e-55;
Matches 157; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

QY 2 EVQLVSGGGVVRPGSLRLSCAASGFTPDYGMVWROAPGKLEWVGGINNGSGTGY 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 EVQLVSGGGGLVPPGSLRLSCAASGFTPDYGMVWROAPGKLEWVGISFGSTTY 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 ADSVKGRFTISRDNKNSLYLQNSIRAEEDTAVYICARRM---APVIWGQTLTVTSRGG 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 ADSVKGRFTISRDNKNSLYLQNSIRAEEDTAVYICARRMGEADAFDIWGQTVTVSSGG 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 GSGGGGGGGGGSS-ELTPDPA-VSVALGQTVRITQGSLSRYSWYQKPPQAPVLV 176
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 GSGGGGGGGGGSDIVWTQSPSTLSASVGDRAVITCRASBGIVHMLAWYQKPKAPKL 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPVGGT 236
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 183 IYKASSLSAGAPRFRFSGSGADFTLITSLQPDDEATYYC---QQYSNYPVLTGGG 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 237 V 237
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 V 241

RESULT 13
US-08-918-148-76
/ Sequence 76, Application US/08918148A
/ Patent No. 6342220
/ GENERAL INFORMATION:
```

APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 76
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
US-08-918-148-76

Query Match 59.2%; Score 771.5; DB 3; Length 245;
Best Local Similarity 63.2%; Pred. No. 1.1e-54;
Matches 153; Conservative 31; Mismatches 51; Indels 7; Gaps 4;

QY 2 EVOLVSGGAVRPGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSTGY 61
DB 3 EVOLVSGGAVRPGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSTGY 62
QY 62 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPV---IMGGTLVTVSRGG 118
DB 63 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMDGSGMDVWGRGTWTVSSGG 122
QY 119 GSGGGGGGGGSSS-ELTQDPA-VSYALGQTVRITTCGDSLRSYASWYQKRGQAPLVY 176
DB 123 GSGGGGGGGGSSDQWTPSPSTLSASIGDRVITTCASRGIIYHMLAWYQKRGKAPKLL 182
QY 177 IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKL 236
DB 183 IYKASSLASGAPSRFSGSGSDPTLTITSLQPDPAFYVC--QOYSNYPITFGGKTL 240
QY 237 VL 238
DB 241 IL 242

RESULT 14
US-09-138-091A-74
Sequence 74; Application US/09138091A
Patent No. 6737249
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: 9491-013-27
CURRENT APPLICATION NUMBER: US/09/138,091A
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: US 60/056,736
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-74

Query Match 59.2%; Score 771.5; DB 4; Length 245;
Best Local Similarity 63.2%; Pred. No. 1.1e-54;
Matches 153; Conservative 31; Mismatches 51; Indels 7; Gaps 4;
QY 2 EVOLVSGGAVRPGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSTGY 61
DB 3 EVOLVSGGAVRPGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSTGY 62

QY 62 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPV---IMGGTLVTVSRGG 118
DB 63 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMDGSGMDVWGRGTWTVSSGG 122
QY 119 GSGGGGGGGGSSS-ELTQDPA-VSYALGQTVRITTCGDSLRSYASWYQKRGQAPLVY 176
DB 123 GSGGGGGGGGSSDQWTPSPSTLSASIGDRVITTCASRGIIYHMLAWYQKRGKAPKLL 182
QY 177 IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKL 236
DB 183 IYKASSLASGAPSRFSGSGSDPTLTITSLQPDPAFYVC--QOYSNYPITFGGKTL 240
QY 237 VL 238
DB 241 IL 242

RESULT 15
US-08-918-148-78
Sequence 78; Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 78
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
FEATURE:
NAME/KEY: unknown
LOCATION: 208
OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match 59.0%; Score 768.5; DB 3; Length 245;
Best Local Similarity 63.5%; Pred. No. 1.9e-54;
Matches 153; Conservative 29; Mismatches 52; Indels 7; Gaps 4;

QY 2 EVOLVSGGAVRPGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSTGY 61
DB 3 EVOLVSGGAVRPGSLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSTGY 62
QY 62 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPV---IMGGTLVTVSRGG 118
DB 63 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMDGSGMDVWGRGTWTVSSGG 122
QY 119 GSGGGGGGGGSSS-ELTQDPA-VSYALGQTVRITTCGDSLRSYASWYQKRGQAPLVY 176
DB 123 GSGGGGGGGGSSDQWTPSPSTLSASIGDRVITTCASRGIIYHMLAWYQKRGKAPKLL 182
QY 177 IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKL 236
DB 183 IYKASSLASGAPSRFSGSGSDPTLTITSLQPDPAFYVC--QOYSNYPITFGGKTL 240
QY 237 V 237
DB 241 I 241

Search completed: April 25, 2005, 21:12:15
Job time : 38.9091 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: April 25, 2005, 20:22:46 ; Search time 108.818 Seconds
(without alignments)
752.325 Million cell updates/sec

Title: US-10-029-926D-208

Perfect score: 1303
Sequence: 1 MEVQLVESGGGVVPGGSLR.....VVEGGGKTLVIGGGCKAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications_AA:*

2: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*

3: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*

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20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260.5	96.7	266	US-10-032-037B-204	Sequence 204, App
2	1260.5	96.7	266	US-10-029-988B-204	Sequence 204, App
3	1260.5	96.7	266	US-10-032-423A-204	Sequence 204, App
4	1257	96.5	277	US-10-032-037B-25	Sequence 25, App1
5	1257	96.5	277	US-10-029-988B-25	Sequence 25, App1
6	1257	96.5	277	US-10-032-423A-25	Sequence 25, App1
7	1257	96.5	277	US-10-029-926B-25	Sequence 25, App1
8	1233	94.6	277	US-10-032-037B-203	Sequence 203, App
9	1233	94.6	277	US-10-029-988B-203	Sequence 203, App
10	1233	94.6	277	US-10-032-423A-203	Sequence 203, App
11	1233	94.6	277	US-10-029-926B-203	Sequence 203, App
12	1218.5	93.5	239	US-09-880-748-937	Sequence 937, App
13	1218.5	93.5	239	US-10-293-418-937	Sequence 937, App

14	1212.5	93.1	239	10	US-09-880-748-2038	Sequence 2038, App
15	1212.5	93.1	239	15	US-10-293-418-2038	Sequence 2038, App
16	1205.5	92.5	280	17	US-10-880-922-6	Sequence 6, App1
17	1196.5	91.8	280	17	US-10-880-922-5	Sequence 5, App1
18	1196.5	91.8	280	17	US-10-880-922-56	Sequence 56, App1
19	1195.5	91.7	280	17	US-10-880-922-60	Sequence 60, App1
20	1192.5	91.5	280	17	US-10-880-922-61	Sequence 61, App1
21	1191.5	91.4	239	15	US-09-880-748-2015	Sequence 2015, App
22	1191.5	91.4	239	15	US-10-293-418-2015	Sequence 2015, App
23	1191.5	91.4	280	17	US-10-880-922-55	Sequence 55, App1
24	1178	90.4	244	14	US-10-322-673-42	Sequence 42, App1
25	1178	90.4	309	13	US-10-052-798-9	Sequence 9, App11
26	1178	90.4	309	14	US-10-288-917-9	Sequence 9, App11
27	1178	90.4	309	15	US-10-423-448-9	Sequence 9, App11
28	1139.5	87.5	239	10	US-09-880-748-2018	Sequence 2018, App
29	1139.5	87.5	239	15	US-10-293-418-2018	Sequence 2018, App
30	1133	87.0	244	14	US-10-322-673-45	Sequence 45, App1
31	1132.5	86.9	239	10	US-09-880-748-2035	Sequence 2035, App
32	1132.5	86.9	239	15	US-10-293-418-2035	Sequence 2035, App
33	1131.5	86.8	245	14	US-10-322-673-43	Sequence 43, App1
34	1131	86.8	252	10	US-09-880-748-1416	Sequence 1416, App
35	1131	86.8	252	15	US-10-293-418-1416	Sequence 1416, App
36	1129.5	86.7	243	17	US-10-935-290-69	Sequence 69, App1
37	1127.5	86.5	243	10	US-09-880-748-2056	Sequence 2056, App
38	1127.5	86.5	243	15	US-10-293-418-2056	Sequence 2056, App
39	1126.5	86.5	239	10	US-09-880-748-2023	Sequence 2023, App
40	1126.5	86.5	239	15	US-10-293-418-2023	Sequence 2023, App
41	1121	86.0	242	17	US-10-935-290-130	Sequence 130, App
42	1119	85.9	240	10	US-09-880-748-2013	Sequence 2013, App
43	1119	85.9	247	10	US-10-293-418-2013	Sequence 2013, App
44	1117.5	85.8	247	10	US-09-880-748-996	Sequence 996, App
45	1117.5	85.8	247	15	US-10-293-418-996	Sequence 996, App

ALIGNMENTS

RESULT 1

US-10-032-037B-204

Sequence 204, Application US/100320378

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOETTES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 204

LENGTH: 266

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-037B-204

Query Match 96.7%; Score 1260.5; DB 15; Length 266;

Best Local Similarity 98.4%; Pred. No. 2,4e-82;

Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY	2	EVQLVSSGGGVVPGGSLRISCAASGFTPDYKMSVVRQAPGGLGEMVSGINNGSGTGY 61
DB	23	EVQLVSSGGGVVPGGSLRISCAASGFTPDYKMSVVRQAPGGLGEMVSGINNGSGTGY 82
QY	62	ADSVKRFITSRNNAKNSLYLQNSRAEDTAVYYCAKRRAPVIMOGTLVTVSRGGGGS 121
DB	83	ADSVKRFITSRNNAKNSLYLQNSRAEDTAVYYCAKRRAPVIMOGTLVTVSRGGGGS 142
QY	122	GGGSGGGGSSSETLQPAVVALGQTVRITCGDLSRSYYASVYQKPGQAPLVLYGKN 181
DB	143	GGGSGGGGSSSETLQPAVVALGQTVRITCGDLSRSYYASVYQKPGQAPLVLYGKN 202


```

Oy      182  NRPGGIDPRFGSSSGNTASLTITGAQAEADYDYNCSRPSGSHVFFGGGKLTIVGGG 241
Db      203  NRPGGIDPRFGSSSGNTASLTITGAQAEADYDYNCSRPSGSHVFFGGGKLTIV- 261

Oy      242  GCKAK 246
Db      262  AAKAK 266

RESULT 2
US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-029-988B-204

```

[illegible]

Query Match	Similarity	96.7%	Score 1260.5	DB 15	Length 266
Best Local	Similarity	98.4%	Pred. No. 2.4e-82		
Matches	Conservative	0	Mismatches	3	Indels
					Gaps
QY	2	EVQLVESGGGVVPPGSGSLRLSCAASGFTPDYGMNWVRQAPGKLEWVSGINWGSGSTGY	61		
Db	23	EVQLVESGGGVVPPGSGSLRLSCAASGFTPDYGMNWVRQAPGKLEWVSGINWGSGSTGY	82		
QY	62	ADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAEMRAPVINGGQTLVTSRGGGS	121		
Db	83	ADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAEMRAPVINGGQTLVTSRGGGS	142		
QY	122	GGGSGGGGSSSLTDDPAVSVALGQTVITTCQGSLSRYASWYQKRGQAPVLYIYKKN	181		
Db	143	GGGSGGGGSSSLTDDPAVSVALGQTVITTCQGSLSRYASWYQKRGQAPVLYIYKKN	202		
QY	182	NRPSGIPRFSSSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPGGKTLVLLGGG	241		
Db	203	NRPSGIPRFSSSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPGGKTLVLLGA	261		
QY	242	GCKAK			
Db	262	AAKAK			

```

RESULT 4
US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match          96.5%; Score 12571, DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4,5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 3
US-10-032-423A-204
/ Sequence 204, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATEATED
/ TITLE OF INVENTION: MOETILES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032,423A
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266

```

Qy	2	EVOLVESGGVVRPGSGRLTSCAASGFTFDDYGMSTMWQAQPGKLEWVSGINMNGSGTGY	61
Db	23	EVQLVESGGGVVRPGSGRLTSCAASGFTFDDYGMSTMWQAQPGKLEWVSGINMNGSGTGY	82
Qy	62	ADSVYKGRFTISRDNAKNSLYIQMNSLRAREDPAVYYCARRAPVYWGGDTLVTSRSGGGGS	121
Db	83	ADSVYGRFTISRDNAKNSLYIQMNSLRAREDPAVYYCARRAPVYWGGDTLVTSRSGGGGS	142
Qy	122	GGGGSGGGSSRLTDPPAVSVVALGGTVAITTCQGDLSRSYVSAWYQQRKGQAPVLVIYGN	181
Db	143	GGGGSGGGSSRLTDPPAVSVVALGGTVAITTCQGDLSRSYVSAWYQQRKGQAPVLVIYGN	202
Qy	182	NRPSGIPDRFGSGSSGNTASLTITGQAQAEADADYYCNSRDSGNNHVFGGTYKLTVLG	239
Db	203	NRPSGIPDRFGSGSSGNTASLTITGQAQAEADADYYCNSRDSGNNHVFGGTYKLTVLG	260


```
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-029-988B-25
```

```
Query Match          96.5%; Score 1257; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGTGY 61
DB 23 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGTGY 82
QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 121
DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 142
QY 122 GGGSGGGGSSSELTQDPDAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKN 181
DB 143 GGGSGGGGSSSELTQDPDAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKN 202
QY 182 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKLTVLG 239
DB 203 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKLTVLG 260
```

```
RESULT 6
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-032-423A-25
```

```
Query Match          96.5%; Score 1257; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGTGY 61
DB 23 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGTGY 82
QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 121
DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 142
```

```
QY 122 GGGSGGGGSSSELTQDPDAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKN 181
DB 143 GGGSGGGGSSSELTQDPDAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKN 202
QY 182 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKLTVLG 239
DB 203 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKLTVLG 260
```

```
RESULT 7
US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-029-926B-25
```

```
Query Match          96.5%; Score 1257; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGTGY 61
DB 23 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGTGY 82
QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 121
DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 142
QY 122 GGGSGGGGSSSELTQDPDAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKN 181
DB 143 GGGSGGGGSSSELTQDPDAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLYIGKN 202
QY 182 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKLTVLG 239
DB 203 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGGTKLTVLG 260
```

```
RESULT 8
US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-032-037B-203
```

```
Query Match          94.6%; Score 1233; DB 15; Length 277;
Best Local Similarity 97.9%; Pred. No. 2.3e-80;
```



```
; Sequence 937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-937

Query Match          93.5%; Score 1218.5; DB 10; Length 239;
Best Local Similarity 97.9%; Pred. No. 2.2e-79;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 61
DB 1 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAARM-APVINGQGITLVVSRGGG 120
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAARRRYALDYWGQGITLVVSRGGG 120
QY 121 SGGGSGGGGSSSELTQDPANVVALGQTVRTTCQDSLSRYSYASWYQOKPGQAPVLVIYK 180
DB 121 SGGGSGGGGSSSELTQDPANVVALGQTVRTTCQDSLSRYSYASWYQOKPGQAPVLVIYK 180
QY 181 NNRPISGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLVILG 239
DB 181 NNRPISGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLVILG 239

RESULT 13
US-10-293-418-937
; Sequence 937, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
```

```
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-937

Query Match          93.5%; Score 1218.5; DB 15; Length 239;
Best Local Similarity 97.9%; Pred. No. 2.2e-79;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 61
DB 1 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAARM-APVINGQGITLVVSRGGG 120
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAARRRYALDYWGQGITLVVSRGGG 120
QY 121 SGGGSGGGGSSSELTQDPANVVALGQTVRTTCQDSLSRYSYASWYQOKPGQAPVLVIYK 180
DB 121 SGGGSGGGGSSSELTQDPANVVALGQTVRTTCQDSLSRYSYASWYQOKPGQAPVLVIYK 180
QY 181 NNRPISGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLVILG 239
DB 181 NNRPISGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLVILG 239

RESULT 14
US-09-880-748-2038
; Sequence 2038, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2038

Query Match          93.1%; Score 1212.5; DB 10; Length 239;
Best Local Similarity 97.5%; Pred. No. 5.9e-79;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 61
DB 1 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAARM-APVINGQGITLVVSRGGG 120
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAARRRYALDYWGQGITLVVSRGGG 120
QY 121 SGGGSGGGGSSSELTQDPANVVALGQTVRTTCQDSLSRYSYASWYQOKPGQAPVLVIYK 180
DB 121 SGGGSGGGGSSSELTQDPANVVALGQTVRTTCQDSLSRYSYASWYQOKPGQAPVLVIYK 180
QY 181 NNRPISGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLVILG 239
```

Db 181 NNRPSGIPDRFSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 239

RESULT 15
US-10-293-418-2038
; Sequence 2038, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2038

Query Match 93.1%; Score 1212.5; DB 15; Length 239;
Best Local Similarity 97.5%; Pred. No. 5.9e-79;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 2 EVOLVESGGGVVRPGSGLRLSCAASGFTPDYGMSTWROAPGKLEWVSGINWNGSTGY 61
Db 1 EVOLVESGGGVVRPGSGLRLSCAASGFTPDYGMSTWROAPGKLEWVSGINWNGSTGY 60
QY 62 ADSVKGRFTISRDNKNSLTLOMNSLRADTAAYVYCARMR-APVIWGQGLTVTVSRGGGG 120
Db 61 ADSVKGRFTISRDNKNSLTLOMNSLRADTAAYVYCARRRYALDYWGQGLTVTVSSGGGG 120
QY 121 SGGGGSGGGSSSELTQDPAVSVALGQTVRIITCOGDSLRSYYASWYQKPGQAPVLYYIK 180
Db 121 SGGGGSGGGSSSELTQDPAVSVALGQTVRIITCOGDSLRSYYASWYQKPGQAPVLYYIK 180
QY 181 NNRPSGIPDRFSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 239
Db 181 NNRPSGIPDRFSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGCTKLTVLG 239

Search completed: April 25, 2005, 21:09:49
Job time : 109.818 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 28.3636 Seconds

(Without alignments)
834.495 Million cell updates/sec

Title: US-10-029-926d-208

Perfect score: 1303
Sequence: 1 MEVQLVESGGGVVPRGSLR.....VVFGGGKLTVLGGGCKAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	44.3	268	A56446	Ig heavy chain V r
2	568	43.6	109	S19663	Ig lambda chain V
3	562	43.1	108	S47184	Ig lambda chain V
4	561.5	43.1	249	S41374	Ig lambda chain Fv an
5	551.5	42.3	110	S36272	Ig lambda chain V
6	546	41.9	137	S70444	Ig lambda chain pr
7	541	41.5	108	S38498	Ig lambda chain -
8	539	41.4	109	S38496	Ig lambda chain -
9	530	40.7	233	S25748	Ig lambda chain -
10	527	40.4	108	L3HUSH	Ig lambda chain V-
11	522.5	40.1	233	JC5322	p53 specific singl
12	518.5	39.8	110	S19672	Ig lambda chain V-
13	517.5	39.7	146	S02083	Ig lambda chain V-
14	513	39.4	98	S26928	Ig heavy chain V r
15	510.5	39.2	128	S31595	Ig heavy chain V r
16	503	38.6	96	S13726	Ig lambda chain -
17	503	38.6	115	S13726	Ig lambda chain V
18	502	38.5	121	S31118	Ig heavy chain - h
19	502	38.5	123	S30532	Ig heavy chain V r
20	502	38.5	233	S25741	Ig lambda chain -
21	501	38.4	121	S31104	Ig heavy chain (su
22	495.5	38.0	112	PH1654	Ig heavy chain V r
23	491	37.7	120	S36273	Ig heavy chain V r
24	488	37.5	134	S31699	Ig heavy chain V r
25	487	37.4	138	S31666	Ig heavy chain V r
26	485.5	37.3	120	S44111	Ig heavy chain V-D
27	485.5	37.3	145	S11239	Ig heavy chain V r
28	485	37.2	119	S31108	Ig heavy chain - h
29	485	37.2	160	S05271	Ig heavy chain pre

30	484.5	37.2	120	S48798	Ig heavy chain V r
31	482	37.0	119	S31107	Ig heavy chain - h
32	480	36.8	121	I55673	Ig heavy chain - h
33	480	36.8	123	S31114	Ig heavy chain - h
34	478	36.7	119	D36005	Ig heavy chain V r
35	477	36.6	140	S31686	Ig heavy chain V r
36	476	36.5	119	C36005	Ig heavy chain V r
37	475	36.5	139	I37781	Ig variable region
38	473.5	36.3	124	S20782	Ig heavy chain V r
39	473.5	36.3	128	S26790	Ig heavy chain V r
40	473.5	36.3	140	S70442	Ig heavy chain pre
41	473.5	36.3	151	A60943	Ig heavy chain pre
42	473	36.3	127	S38489	Ig heavy chain - h
43	472	36.3	135	S31598	Ig heavy chain V r
44	472	36.2	98	S26927	Ig heavy chain V r
45	472	36.2	143	S23524	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C/Species: Mus musculus (house mouse)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C/Accession: A56446
R/Ting, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident
A/Reference number: A56446; PMID:95229583; PMID:7713873
A/Accession: A56446
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-268 <TN>
A/Cross-references: GB:U20617
C/Keywords: heterotetramer; immunoglobulin

Query Match 44.3%; Score 577; DB 2; Length 268;
Best Local Similarity 50.2%; Pred. No. 1.3e-32;
Matches 121; Conservative 34; Mismatches 78; Indels 8; Gaps 5;

QY	2	EVQLVESGGGVVPRGSLRSCAASGFTPDYGMVWRQAPGKLEIVSGINNCGSTGY	61
DB	3	QVTLQSSGAEIVPRGASVSLCTSGFNIDTMMHVKQREGLERIGRIAPANGITKY	62
QY	62	ADSVKGRFTISRDNAKNSLYLNQSIRAEEDTAVYICAR--MRAPVIWGGLVTVSRGG	118
DB	63	DPFGKATIAADVTSSNTAVLQSLTSEDTAVYICASYLTRYENVWGGLTVTVSSGG	122
QY	119	GGSGGGSGSGGGSGS-ELTQDPVAV-SVALGQTVARITCGDSLRSYVSWYQKQCAPVIV	176
DB	123	GGSGGGSDSGGGSDIELTQSPALMSASLGKVTMSGRASSVAV-FIYVQOKSDASPKW	181
QY	177	IYCKNRPSPGIPDPFGSSSGNTASLTITGAQEADEADYVCNRSNGNHWVGGGKTLT	236
DB	182	VYTSHPFQVPRFSGSGSGNSYLTISMEGEDATYTCQPTSS--PFTGSGTKLE	239
QY	237	V 237	
DB	240	I 240	

RESULT 2

S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19663
R/Marx, U.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter
J. Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p
A/Reference number: S19663; PMID:92085276; PMID:1748994

A/Accession: S19663
 A/Molecule type: mRNA
 A:Residues: 1-109 <MAR>
 A:Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.6%; Score 568; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2,2e-32;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVIYGNRPPSGIPDR 190
 Db 1 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVIYGNRPPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTTLTVL 239
 Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTTLTVL 109

RESULT 3

S47184
 Ig lambda chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S47184
 R/McInosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
 Submitted to the EMBL Data Library, June 1994
 A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
 A/Reference number: S47181
 A/Accession: S47184
 A/Status: preliminary
 A/Molecule type: mRNA
 A:Residues: 1-108 <MCI>
 A:Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 562; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 5.5e-32;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVIYGNRPPSGIPDR 190
 Db 1 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVIYGNRPPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTTLTVL 238
 Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTTLTVL 108

RESULT 4

S41374
 single chain Fv antibody - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C/Accession: S41374
 R/Atsienko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
 Submitted to the EMBL Data Library, January 1994
 A/Description: Construction and functional characterization of a single chain Fv antibody
 A/Reference number: S41374
 A/Accession: S41374
 A/Status: preliminary
 A/Molecule type: DNA
 A:Residues: 1-249 <ART>
 A:Cross-references: EMBL:Z29480

Query Match 43.1%; Score 561.5; DB 2; Length 249;
 Best Local Similarity 48.6%; Pred. No. 1.4e-31;
 Matches 121; Conservative 36; Mismatches 71; Indels 21; Gaps 6;

QY 2 EVQLVESGGGVYRPGGSLRLSCAASGFTEDYGMGVRQAPGKGLRWISGINMGSTGY 61
 Db 1 QVQLQSGAEALVRPGASVLTCTASGFNFKDYLHVVKQRPKGLLEWIRIAPASGNVYK 60
 QY 62 ADSVKRFTISDNKNSLYLQNSLRADPTVYCAR----MRAVIMGQGLTVVSRG 117
 Db 61 VPRFQKATITADTSSNTAVYLLSLTSDTLYVYCARPDLYTSLGVWGQSTVTVSR 120
 QY 118 GGGSGGGSGGGSS-ELTQD--PAVVALGQTVRITTCQ-----GDSLRSYASWYQ 166
 Db 121 GGGSGGGSGGGSDLELTQSPSVVIRGESVTSICRSKSLTYSDDG-----YLFWFL 176
 QY 167 QRPQAPVLVIYGNRPPSGIPDRSGSSGNTASLTITGAQAEDEADYYCNSRDSGNN 226
 Db 177 QRPQAPVLVIYGNRPPSGIPDRSGSSGNTASLTITGAQAEDEADYYCNSRDSGNN 234
 QY 227 VPRFGGKTTL 235
 Db 235 LTFGAGTKL 243

RESULT 5

S36272
 Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 C/Accession: S36272
 R/Giffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBD J. 12, 725-734, 1993
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.
 A/Reference number: S36256; NID:93178448; PMID:7679990
 A/Accession: S36272
 A/Status: preliminary
 A/Molecule type: mRNA
 A:Residues: 1-110 <GRI>
 A:Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g933912
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 551.5; DB 2; Length 110;
 Best Local Similarity 98.2%; Pred. No. 2.9e-31;
 Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 131 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVIYGNRPPSGIPDR 190
 Db 1 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVIYGNRPPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTTLTVL 239
 Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTTLTVL 110

RESULT 6

S70444
 Ig lambda chain precursor V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C/Accession: S70444; S70426
 R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
 Mol. Immunol. 29, 1363-1373, 1992
 A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of F
 A/Reference number: S70442; PMID:93024508; PMID:1383695
 A/Accession: S70444

A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A:Residues: 1-127 <CUI>
 A:Cross-references: UNIPROT:Q9NSD6
 A/Experimental source: clone E29.1
 R/Tonnelie, C.

Submitted to the EMBL Data Library, May 1990
 A/Reference number: S70426
 A/Accession: S70426

A:Molecule type: mRNA
 A:Residues: 1-90 <TON>
 A:Cross-references: EMBL:X53070
 A:Experimental source: cell line E29.1, clone VL 29-1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
 F:14-108/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 546; DB 2; Length 127;
 Best Local Similarity 97.2%; Pred. No. 8.1e-31;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 131 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 190
 |||||
 DB 20 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 79

QY 191 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 238
 |||||
 DB 80 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 127

RESULT 7

Ig lambda chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S38498
 R:Mark, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
 submitted to the EMBL Data Library, June 1993
 A:Description: Human antibody fragments specific for human blood group antigens from a F
 A:Reference number: S38488
 A:Accession: S38498
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <MAR>
 A:Cross-references: EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; PID:G414044
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 41.5%; Score 541; DB 2; Length 108;
 Best Local Similarity 97.2%; Pred. No. 1.5e-30;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 132 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 191
 |||||
 DB 1 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 60

QY 192 SSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 239
 |||||
 DB 61 SSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 108

RESULT 8

Ig lambda chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S38496
 R:Mark, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
 submitted to the EMBL Data Library, June 1993
 A:Description: Human antibody fragments specific for human blood group antigens from a F
 A:Reference number: S38488
 A:Accession: S38496
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <MAR>
 A:Cross-references: EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PID:G414040
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 41.4%; Score 539; DB 2; Length 109;
 Best Local Similarity 93.6%; Pred. No. 2.1e-30;
 Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 131 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 190
 |||||
 DB 1 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 239
 |||||
 DB 61 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 109

RESULT 9

Ig lambda chain - human
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S25748
 R:Comitato, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin la
 A:Reference number: S16439; MUID:91257162; PMID:1904362
 A:Accession: S25748
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-233 <COM>
 A:Cross-references: EMBL:X57813; NID:G33725; PIDN:CAA0950.1; PID:G33726
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 40.7%; Score 530; DB 2; Length 233;
 Best Local Similarity 91.7%; Pred. No. 1.9e-29;
 Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 131 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 190
 |||||
 DB 20 SSELTOPPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPVLYYGKNNRPSGIPDR 79

QY 191 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 239
 |||||
 DB 80 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGTYLTVLG 128

RESULT 10

Ig lambda chain V-II region (Sh) - human
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A01980
 R:Tilani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
 J. Biol. Chem. 245, 2171-2176, 1970
 A>Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complet
 A:Reference number: A92057; MUID:70166723; PMID:4909564
 A:Accession: A01980
 A:Molecule type: protein
 A:Residues: 1-108 <TIT>
 A:Cross-references: UNIPROT:P01714
 A>Note: the sequence of the C region is also given

C:Genetics:
 A:Gene: IGLV6
 A:Cross-references: GDB:119342; OMIM:147240
 A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>
 F:21-86/Disulfide bonds: #status experimental

Query Match 40.4%; Score 527; DB 1; Length 108;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 127.091 Seconds
(without alignments)
991.192 Million cell updates/sec

Title: US-10-029-926D-208
Perfect score: 1303
Sequence: 1 MEQVLVSSGGVVRPGSLR.....VFFGGTKLTVLGGGCKAK 246

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	58.2	240	2 Q65ZC9	Q65ZC9 homo sapien
2	715	54.9	255	2 Q6KBO5	Q6KBO5 mus musculu
3	700.5	53.8	248	2 Q65ZG7	Q65ZG7 mus sp. b3(
4	682.5	52.4	298	2 Q9QYF0	Q9QYF0 Eynthetic c
5	636	48.8	244	2 Q65ZC8	Q65ZC8 homo sapien
6	600	46.0	241	2 Q921A6	Q921A6 mus musculu
7	578	44.4	243	2 Q7TOM2	Q7TOM2 mus musculu
8	552	42.4	107	2 Q9NSD6	Q9NSD6 homo sapien
9	550.5	42.2	112	2 Q9HCC1	Q9HCC1 homo sapien
10	547	42.0	487	2 Q65ZL2	Q65ZL2 mus sp. fv/
11	530	40.7	233	2 Q6GMW4	Q6GMW4 homo sapien
12	527	40.4	108	1 LV3A_HUMAN	P01714 homo sapien
13	512	39.3	472	2 Q6N089	Q6N089 homo sapien
14	510	39.1	499	2 Q8NSK4	Q8NSK4 homo sapien
15	504	38.7	573	2 Q8M3J8	Q8M3J8 homo sapien
16	498.5	38.3	218	2 Q92S51	Q92S51 mus musculu
17	483	37.1	121	2 Q9UL71	Q9UL71 homo sapien
18	476	36.5	470	2 Q6PJ44	Q6PJ44 homo sapien
19	476	36.5	478	2 Q6PI81	Q6PI81 homo sapien
20	476	36.5	606	2 Q6GMW2	Q6GMW2 homo sapien
21	473	36.3	613	2 Q8M3J8	Q8M3J8 homo sapien
22	472.5	36.3	597	2 Q96BB9	Q96BB9 homo sapien
23	472	36.2	464	2 Q6MZU6	Q6MZU6 homo sapien
24	470	36.1	113	2 Q9UL90	Q9UL90 homo sapien
25	465.5	35.7	493	2 Q6GMW2	Q6GMW2 homo sapien
26	464	35.6	493	2 Q6GMW2	Q6GMW2 homo sapien
27	461.5	35.4	478	2 Q9UL91	Q9UL91 homo sapien
28	456.5	35.0	475	2 Q6MZU6	Q6MZU6 homo sapien
29	455	34.9	466	2 Q6IN78	Q6IN78 homo sapien
30	452.5	34.7	479	2 Q6MZV6	Q6MZV6 homo sapien
31	446.5	34.3	116	1 HV3T_HUMAN	P01781 homo sapien

32	444.5	34.1	122	1 HV3G_HUMAN	P01768 homo sapien
33	444	34.1	116	2 Q9UL93	Q9UL93 homo sapien
34	444	34.1	473	2 Q91Z05	Q91Z05 mus musculu
35	442.5	34.0	465	2 Q6PC4	Q6PC4 homo sapien
36	442	33.9	117	1 HV3C_HUMAN	P01764 homo sapien
37	440.5	33.8	494	2 Q96K68	Q96K68 homo sapien
38	438.5	33.7	483	2 Q6MZX9	Q6MZX9 homo sapien
39	438.5	33.7	494	2 Q6ZW64	Q6ZW64 homo sapien
40	438.5	33.7	544	2 Q6PJ95	Q6PJ95 homo sapien
41	438	33.6	479	2 Q91WP5	Q91WP5 mus musculu
42	436.5	33.5	118	2 Q9UL72	Q9UL72 homo sapien
43	436.5	33.5	475	2 Q6GMW7	Q6GMW7 homo sapien
44	434	33.3	233	2 Q8TBC9	Q8TBC9 homo sapien
45	434	33.3	480	2 Q6N094	Q6N094 homo sapien

ALIGNMENTS

RESULT 1

ID	Q65ZC9	PRELIMINARY:	PRT:	240 AA.
AC	Q65ZC9;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Single-chain Fv (Fragment).			
GN	Name=ScFv;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C1q/7;			
RX	MEDLINE=97362799; Pubmed=9219263;			
RA	Kontermann R.E., Wing M.G., Winter G.;			
RT	"Complement recruitment using bispecific diabodies.";			
RL	Nat. Biotechnol. 15:629-631(1997).			
DR	EMBL; Y13056; CAJ73499.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_2.			
DR	SMART; SM00409; IG_2.			
DR	SMART; SM00406; IG_V_2.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
FT	NON_TER 1			
FT	NON_TER 240			
SQ	SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;			

Query Match 58.2%; Score 758; DB 2; Length 240;
Best local similarity 62.9%; Pred. No. 1,8e-47;
Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;

QY	2 EVOLVSGGCVVRPGSLRISCAASGTFPDYGMWVRQPGGLEVVSINNNGSTGY 61
DB	1 QVULVSGGGLVOPGSLRISCAASGTFSSYGMWVRQPGGLEVVAIVISDGSWKY 60
QY	62 ADVKGRFTISRANAKSLYLQNNSLRAEDTAVYYCAKMPAYI--WGQGLTVVSRGGG 119
DB	61 ADVKGRFTISRANAKSLYLQNNSLRAEDTAVYYCARMDGSLDLPKGGKTLTVVSGGG 120
QY	120 GSGGGGSGGGGSS-ELTQDPA-VSVALGQTVRTTCQDLSRSYYASWYQKPGQAPYLV 177
DB	121 GSGGGGSGGGGSDIOWTQSPSTIASIGDVIITTCASSEGIVRWLAWYQKPGKAPYDL 180
QY	178 YGNRRPSGIPDRFSSSSGNTASLTITGAQAEADADYVNSDSSGNHVPFGGRTLV 237
DB	181 YKASLSLRAPSRFSGSGSDFTLTISLQPDPAFYTC--QQVSNYPLTPEGGTLRI 238

RESULT 2

Q6KB05 PRELIMINARY; PRT; 255 AA.
 ID Q6KB05
 AC Q6KB05;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE SCFV B8E5 protein (Fragment).
 GN Name=SCFV B8E5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/c;
 RA Briand J.P., Hoebeke J., Tugler J., Maurice D., Roegel J.C.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ746180; CAG34081.1; -
 DR HSSP; P01837; 1KCR.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGv; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
 Query Match 54.9%; Score 715; DB 2; Length 255;
 Best Local Similarity 58.8%; Pred. No. 2.6e-44;
 Matches 147; Conservative 33; Mismatches 54; Indels 16; Gaps 6;
 QY 2 EVOLVSGGGVVRPGSLRISCASGTFDDYGMWVRQAPGKLEWVSGINMGSGTGY 61
 DB 1 QVQLQOSGDLVPRGSLKLVSCASGTFSSYGSWVRQTPDKRLIEWVAITIGSGSTYY 60
 QY 62 ADSVKGRTISRDNKNSLYLQMNLSLRADPTAVVYCARM-----RAPVWGQGLTVTVS 115
 DB 61 PDSVKGRTISRDNKNTLYLQMSLSKSEDTAVYCARHINRYDAGFDVWGQGLTVTVS 120
 QY 116 RGGGSGGGSGGGSGGSS-ELTQDP-AVSVALGQTVRTTCQ-GDSL-----RSYASWYQQ 167
 DB 121 SGGSGSGGGSGGGSGGSDIWAQSPSSLSVAGEEVIMSCSSQSLNSRNQKYLAWYQQ 180
 QY 168 KPGQAPLVLYGKNNRPSGTPDRPSSSGSGNTASLTITGAQAEADYVYCNRSRSGNHV 227
 DB 181 KPGQSPKLLIYGASTRESGVDRPTGSGSGTDFTLTISVQAEADLAVYVQNDHS--YPL 238
 QY 228 VFGGSGTKLTV 237
 DB 239 TFGAGTKLEI 248
 RESULT 3
 Q6SZ07 PRELIMINARY; PRT; 248 AA.
 ID Q6SZ07
 AC Q6SZ07;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE B3 (Fv)-PB40 (Fragment).
 GN Name=B3 (Fv)-PB40;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=92020904; PubMed=1924323;
 RA Brinkmann U., Pai L.H., Fitzgerald D.J., Williamson M., Paetan I.,
 RT "B3 (Fv)-PB38DEL, a single-chain immunotoxin that causes complete
 regression of a human carcinoma in mice.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).
 DR EMBL; S57990; AAB19971.2; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGv; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON TER 248
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43B570950 CRC64;
 Query Match 53.8%; Score 700.5; DB 2; Length 248;
 Best Local Similarity 58.0%; Pred. No. 2.8e-43;
 Matches 145; Conservative 32; Mismatches 56; Indels 17; Gaps 6;
 QY 1 MEVQLVSGGGVVRPGSLRISCASGTFDDYGMWVRQAPGKLEWVSGINMGSGTGY 60
 DB 1 MDVQLVSGGGVLRQPGSLKLVSCATSGTFSDYIMVWVRQTPDKRLIEWVAITISNDSSAA 60
 QY 61 YADSVKGRFTISRDNKNSLYLQMNLSLRADPTAVVYCARMRA-----PVIWGQGLTVTVR 116
 DB 61 YSDTVKGRFTISRDNKNTLYLQMSRLKSEDTAVYCARGLAMGAFAYWGQGLTVTVS 120
 QY 117 GGGSGGGSGGGSGGSSSEL-TQDP-AVSVALGQTVRTTCQ-GDSL-----RSYASWYQQXP 169
 DB 121 GGGSGGGSGGGSGGSDVMTQSPSLSPVSLGDAQASICRSGSQTIVHNSNGNTYLEWTLQKP 180
 QY 170 GQAPVLVLYGKNNRPSGTPDRPSSSGSGNTASLTITGAQAEADYVYCNRSRSGNHV-- 227
 DB 181 GQSPKLLIYKNSRFGVDRPSSGSGTDFTLIKISRVEADLVGYC-----FQSGHWPP 236
 QY 228 VFGGSGTKLTV 237
 DB 237 TFGSGTKLEI 246
 RESULT 4
 Q9QYF0 PRELIMINARY; PRT; 298 AA.
 ID Q9QYF0
 AC Q9QYF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CN 8 single chain antibody.
 GN Name=CN 8 scFv;
 OS Synthetic construct.
 OS other sequences; artificial sequences.
 OC NCBI_TaxID=32630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;
 RA Shinozaki N., Demura T., Fukuda H.;
 RT "Isolation of a vascular cell wall-specific monoclonal antibody
 recognizing a cell polarity by using a phage display subtraction
 method.";
 RT method.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
 DR EMBL; AB036341; BAA86633.1; -
 DR PIR; A33933; A33933.
 DR PIR; S19112; S19112.
 DR HSSP; P01820; 1A70.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGv; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON TER 248
 SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
 Query Match 52.4%; Score 682.5; DB 2; Length 298;
 Best Local Similarity 55.7%; Pred. No. 7e-42;
 Matches 137; Conservative 28; Mismatches 64; Indels 17; Gaps 5;
 QY 2 EVOLVSGGGVVRPGSLRISCASGTFDDYGMWVRQAPGKLEWVSGINMGSGTGY 61
 DB 1 QVQLQOSGDLVPRGSLKLVSCASGTFSSYGSWVRQTPDKRLIEWVAITIGSGSTYY 60

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Db      40 QVTLQOOSGGGLVPRGSLKLSLCAASGSDFSRWYMWVROAPGKGLMEIGIINPDSSTINY 99
QY      62 ADSVKRFTISRDNANKSLYLQNSLRABEDTAVYYCARMR---APVIMGGGLTVTSRG 118
Db      100 TBSLKQFTISRDNANKSLYLQNSKVRSEDTALYCARASYGHSAVYGGITVTVSSGG 159
QY      119 GSGSGSGSGSGSSS-ELTODPA-VSVALGQTVRTTCGDSLRSYASWYQKPGQAPLV 176
Db      160 GSGSGSGSGSGSDIELTQSPALSASVGETVITTCASGNINHYLAWYQKQKSPQL 219
QY      177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNBRDSSGNH---VVEGG 231
Db      220 VYNAKTLADVPFRFSGSGSGGTQYSLKINSLOPEDFGSYC-----QHFMTTPYFGG 272
QY      232 GTKLTV 237
Db      273 KLEI 278

RESULT 5
065ZC8      PRELIMINARY;      PRT;      244 AA.
ID 065ZC8
AC 065ZC8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=9362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13057; CAJ73500.1; -.
DR InterPro: IPR003399; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IG; 2.
DR PROSITE: PS0835; IG_LIKE; 2.
DR SMART: SM00406; IG; 2.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match      48.8%; Score 636; DB 2; Length 244;
Best Local Similarity 50.8%; Pred. No. 1,4e-38;
Matches 124; Conservative 46; Mismatches 64; Indels 10; Gaps 4;

QY      2 EVOLVSGGVPRGSLRSLCAASGFTPDYGMWVROAPGKLEWVGGINNGSGTGY 61
Db      1 QVQLVDSGAEVKKPSQSVKSCASGTTFSDDHMYMVRQAPGGGLEMMGWIDPNNQDTRF 60
QY      62 ADSVKRFTISRDNANKSLYLQNSLRABEDTAVYYCAR---MRAPVIMGGGLTVTS 115
Db      61 AQFQGRVTRWTRDTSTISAAVMEVSRLSRSDTAVYYCARSGTSALYGMVWGQGLTVTS 120
QY      116 RGGSGSGSGSGSSS-ELTODPA-VSVALGQTVRTTCGDSLRSYASWYQKPGQAP 173
Db      121 GSGSGSGSGSGSDIQMTQSPSTLSASIGRVTITTCASBGITVIMLAWYQKQKSPKAP 180
QY      174 VLVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNBRDSSGNHVVFGG 233
Db      181 KFLIYKASSLASGAPSRFSGSGSGTDTLTITSLQPDFTVYC---QQYNSYPLTREGGT 238
QY      234 KLTIV 237
Db      239 KLEI 242

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RESULT 6
0921A6      PRELIMINARY;      PRT;      241 AA.
ID 0921A6
AC 0921A6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL: U88067; AAB48044.1; -.
DR PIR: S19965; S19965.
DR PIR: S19967; S19967.
DR PIR: S19968; S19968.
DR PIR: S26325; S26325.
DR HSSP: P01607; 1BMW.
DR SMART: SM00406; IG; 2.
DR PROSITE: PS0835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match      46.0%; Score 600; DB 2; Length 241;
Best Local Similarity 51.9%; Pred. No. 5.6e-36;
Matches 126; Conservative 34; Mismatches 67; Indels 16; Gaps 6;

QY      2 EVOLVSGGVPRGSLRSLCAASGFTPDYGMWVROAPGKLEWVGGINNGSGTGY 61
Db      1 QVTLQOOSGPELKKPGETVAKISCAASGVTFTDYGMMWVROAPGKGLKMGWINTYGEPTY 60
QY      62 ADSVKRFTISRDNANKSLYLQNSLRABEDTAVYYCAR---MRAPVIMGGGLTVTSRG 118
Db      61 ADFKGRFAPSLSTASTALQINLNKNEDTAVYFCARQDLKYPFYWGQGITVTVSSGG 120
QY      119 GSGSGSGSGSGSSS-ELTODP-AVSVALGQTVRTTCGDSLRSYASWYQKPGQAP--- 173
Db      121 GSGSGSGSGSGSDIELTQSPSLASLGKVTITTCASQDINKYIANTQHKRGKPRSA 180
QY      174 -VLVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYVYCNBRDSSGNHVVFGG 232
Db      181 HTLHIYIQ---PGIPSRFSGSGSGRDYFSPISNLEPEDIATVYCLHYD---NLHTFGGG 233
QY      233 TKL 235
Db      234 TKL 236

RESULT 7
07TM2      PRELIMINARY;      PRT;      243 AA.
ID 07TM2
AC 07TM2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE scFv 6H8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;

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[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Balb/C;
RC MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RX Peter J.C., Eftekhar P., Billiald P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor."
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL: AJ574851; CAE00495.1; -.
DR HSSP: P01751; 1A6W.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IG_1.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFP64D2DC4F76 CRC64;
Query Match 44.4%; Score 578; DB 2; Length 243;
Best Local Similarity 49.4%; Pred. No. 2.3e-34;
Matches 118; Conservative 37; Mismatches 78; Indels 6; Gaps 4;
QY 2 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINNGSGTGY 61
DB 1 QVQLQSGSEIVRGASVKISCAASGFTFTTMMHWKQHGQGLEWIGNITPGSGITNY 60
QY 62 ADSVKRFTISRDNANKSLYLQNMNLSRAEDTAVYYCAR-MRAPYWGQGLTVTVSRGGG 120
DB 61 DEKKNKNGILTVDTSSSTAYMHLSLASEDSAVYYCARGRGLDWAGTTLTVSSGGG 120
QY 121 SGGGSGGGGGS-ELTP-DPAVVALDQYTRITCGDSLRSYASVYQKPGAPVLVY 178
DB 121 SGGGSGGGGSDIQMTQSSSFVSICDRVLTCTKASEDIYNRLAWYQKPGAPVLLIS 180
QY 179 GKNNRPSGIDPRFSGSSSGNTASLTINGAEDPADYCYNSRDSGNHVFGGTGLTV 237
DB 181 GATSLTGVPSRPSGSGSKDYTLITSLTQEDVATYYCQGYSTR--TFGGTKLEI 236
RESULT 8
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Homo sapiens This CDS feature is included to show the translation of
DE the corresponding V-region. Presently translation qualifiers on
DE V-region features are illegal. (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocyte;
RA Hohmann A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: I43092; AAA69746.2; -.
DR PIR: S70444; S70444.
DR HSSP: P01709; 2MCG.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IG_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;
Query Match 42.4%; Score 552; DB 2; Length 107;
Best Local Similarity 98.1%; Pred. No. 7.2e-33;
Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 133 ELTDPAVSVAGQTVRITCGDSLRSYASVYQKPGAPVLVYGNKNNRPSGIDPRFS 192

DB 1 ELTDPVSVAGQTVRITCGDSLRSYASVYQKPGAPVLVYGNKNNRPSGIDPRFS 60
QY 193 GSSSGNTASLTITGAQAEADYCYNSRDSGNHVFGGTGLTVLG 239
DB 61 GSSSGNTASLTITGAQAEADYCYNSRDSGNHVFGGTGLTVLG 107
RESULT 9
ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB049915; BAB16829.1; -.
DR HSSP: P01783; 1IGC.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IG_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA5EC3B84788 CRC64;
Query Match 42.2%; Score 550.5; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 9.8e-33;
Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
QY 2 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINNGSGTGY 61
DB 1 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINNGSGTGY 60
QY 62 ADSVKRFTISRDNANKSLYLQNMNLSRAEDTAVYYCAR-MRAPYWGQGLTV 112
DB 61 ADSVKRFTISRDNANKSLYLQNMNLSRAEDTAVYYCARRRYALDWGQGLTV 112
RESULT 10
ID Q65ZL2 PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, last annotation update)
DE Fv/M4.
GN Name=M4-IFN- γ -<tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TRG72 chimeric
RT antibody secreted from myeloma cells."
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL: S82493; AAB37424.2; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.

DR InterPro:IPR003596; Ig_V.
DR Pfam: PF07654; C1-set; 2.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 3.
DR SMART: SM00407; IGC1; 2.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
DR SEQUENCE 487 AA; 53578 MW; C7BAB969F30555504 CRC64;
SO

Query Match 42.0%; Score 547; DB 2; Length 487;
Best Local Similarity 45.8%; Pred. No. 8.7e-32;
Matches 109; Conservative 44; Mismatches 79; Indels 6; Gaps 5;

QY 2 EVLVESGGGVRRPGGSLRLSCAASGFTFDDYSGMSWVRQAGKGLWVSGINWNGSGTGY 61
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 20 QVQLQQSDAEIVKPGASVKISCKASGYFTFDTHAIWMAKQKPEQGLEWIGYISPNDIDIKY 79
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 62 ADSVKGRTTISRDNAKNSLYIQAMSIRREDPAIVYCAAMRAPVIWGQGTLLVTVSRGGGGS 121
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 80 NEKFPGKATLTLPADKSSSTAYVQMLNSLTSEDSAVYFCRKSYYG-HNGQGTLLTG-S-GGGGS 137
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 122 GGGSGGGGGSS-ELRQDPA-VSVALGQIVRTTCQSDLSRSYYASVYQOKPGQAPVLYVYG 179
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 138 GGGSGGGGGSSRIQMTQSPASLSVSNGELVITTCRSENVITYSNLARYQOKGSGPOLVYA 197
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 180 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADVDYCNRSRDSGNNHVFGGGRKLTIV 237
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 198 ATNLADGVPRSPFGSGSGCTGYSLKINLSQSEDFSGSYG-C-QHFMQTPYTFGGGRLEI 253
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
Q6GMW4 PRELIMINARY; PRT; 233 AA.
Q6GMW4
AC Q6GMW4
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
OS Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemien C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepienon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bock S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Holys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smatue D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

	DR	EMBL: BC073786; AAH73786.1; --
	DR	GO: GO:0005489; F:electron transporter activity; IEA.
	DR	GO: GO:0006118; P:electron transport; IEA.
	DR	InterPro: IPR003599; IG.
	DR	InterPro: IPR007110; IG-1like.
	DR	InterPro: IPR003597; IG_C1.
	DR	InterPro: IPR003006; IG_MHC.
	DR	InterPro: IPR003596; IG_v.
	DR	InterPro: IPR006662; ThioRed.
	DR	Pfam: PF07654; C1-set; 1.
	DR	Pfam: PF00047; Ig; 2.
	DR	PRINTS: PR00421; THIOREDOXIN.
	DR	SMART: SMO0409; IG; 2.
	DR	SMART: SMO0407; IGc1; 1.
	DR	SMART: SMO0406; IGV; 1.
	DR	PROSITE: PS50835; IG_LIKE; 2.
	DR	PROSITE: PS00290; IG_MHC; UNKNOWN_1.
	KW	Hypothetical protein.
	SQ	SEQUENCE 233 AA; 24855 MW; 462677B38FDE5BD CRC64;
	Query Match	40.7%; Score 530; DB 2; Length 233;
	Best Local Similarity	91.7%; Pred. No. 6.7e-31;
	Matches 100; Conservative	6; Mismatches 3; Indels 0; Gaps 0
Oy	131	SSSLTQDPAVSVALGQTIVRITTCQGDLSLRSYVASWTQQKPGAPVLIYIGKNRPSPGIIPR 190
Dd	20	SSSLTQDPAVSVALGQTIVRITTCQGDLSLTYYASWTQQKPGAPVLIYIAKDNRPSGPDR 79
Oy	191	FSGSSSGNTASLTITGAQADEADVDYCNSPSSGGHHVPFGGTXTLVLG 239
Dd	80	FSGSGSGNTASLTITGAQADEADVDYCNSRDSSGSHLVFGTITKTATVLG 128

RESULT 12			
LV3A_HUMAN	STANDARD;	PRT;	108 AA.
ID LV3A_HUMAN			
AC P01714;			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, last sequence update)			
DT 05-JUL-2004 (Rel. 44, last annotation update)			
DE Ig lambda chain V-II region SH.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_TaxID=9606;			
[1]			
RP SEQUENCE.			
RX MEDLINE=70166723; PubMed=4909564;			
RA Tiliani K., Wtkler M., Shinoda T., Putnam F.W.;			
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The			
RT complete amino acid sequence and the location of the disulfide			
RT bridges."			
RL J. Biol. Chem. 245:2171-2176(1970).			
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.			
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR PIR; A01980; L3HUSH.			
DR HSSP; P01703; 7FAB.			
DR GO; GO:0005576; C:extracellular; NAS.			
DR GO; GO:0003823; F:antigen binding; NAS.			
DR GO; GO:0006955; P:immune response; NAS.			
DR InterPro; IPR007110; Ig-like.			
DR InterPro; IPR003566; Ig_V.			
DR Pfam; PF00047; Ig; 1.			
DR SMART; SM00406; IGV; 1.			
DR PROSITE; PSS0835; IG_LIKE; 1.			
KW Bence-Jones protein; Direct protein sequencing;			
KW Immunoglobulin V region.			
KM DOMAIN 1 97 Ig-like.			
FT DISULFID 21 86			
FT NON TER 108 108			
SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;			

Query Match 40.4%; Score 527; DB 1; Length 108;

Best Local Similarity 92.6%; Pred. No. 4.8e-31;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 132 SEITOPANVVALGQVTRITCCDSIRSYASYAQQKPGQAPVLYYGNRRPSGIPDR 191
DB 1 SEITOPANVVALGQVTRITCCDSIRSYASYAQQKPGQAPVLYYGNRRPSGIPDR 60
QY 192 SSSSSGNTASLTITGAQAEADYCNRSRDSGNHVFGGTLVTLG 239
DB 61 SSSSSGNTASLTITGAQAEADYCNRSRDSGNHVFGGTLVTLG 108

RESULT 13

Q6N089 PRELIMINARY; PRT; 472 AA.

AC Q6N089, PRELIMINARY; PRT; 472 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp666P15220.
GN Name=DKFZp666P15220;
OS Homo sapiens (human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=FROM N.A.
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
RU Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640627; CA645781.1; -
DR HSSP: P01861; IADQ
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00409; IG_2.
DR SMART: SM00407; IG1; 3.
DR SMART: SM00406; IG1; 1.
DR PROSITE: PS00835; IG_1like; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 39.3%; Score 512; DB 2; Length 472;
Best Local Similarity 48.5%; Pred. No. 3e-29;
Matches 114; Conservative 19; Mismatches 70; Indels 32; Gaps 5;

QY 2 EVOLVSGGAVPVGSLRLSCASGFTPDYKSWTRQAPGKLEWVGSIINNGSTGY 61
DB 20 EVOLVSGGAVPVGSLRLSCASGFTPDYKSWTRQAPGKLEWVGSIINNGSTGY 79
QY 62 ADVKGRFTSRDANKSLYLQNSLRAEPTAVYCAR-----NRAPVINGQTLV 113
DB 80 ADVKGRFTSRDANKSLYLQNSLRAEPTAVYCAR-----NRAPVINGQTLV 139
QY 114 VSRGGGSGGSGGSSSELTPDPAVSVALGQVTRITCCDSIRSYASYAQQKPGQAP 173
DB 140 VS-----SASTKGPVPLAPSKSTSGGTALGC---LVKDYFPE-----P 178
QY 174 VLYYGNRRPSGIPDR-----PDRFGSSGNTASLTITGAQAEADYCNRSRDSGN 225
DB 179 VLYYGNRRPSGIPDR-----PDRFGSSGNTASLTITGAQAEADYCNRSRDSGN 233

RESULT 14
Q6N5K4 PRELIMINARY; PRT; 499 AA.
ID Q6N5K4
AC Q6N5K4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MG27165 protein.
OS Homo sapiens (human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Blood;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.S., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Groomwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalek U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP TISSUE=Blood;
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC032249; AAH32249.1; -
DR HSSP: P01876; IOWO.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-set; 2.
DR Pfam: PF00047; IG1; 1.
DR SMART: SM00406; IG1; 1.
DR PROSITE: PS00835; IG_1like; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 39.1%; Score 510; DB 2; Length 499;
Best Local Similarity 51.3%; Pred. No. 4.4e-29;
Matches 120; Conservative 14; Mismatches 42; Indels 58; Gaps 8;

QY 2 EVOLVSGGAVPVGSLRLSCASGFTPDYKSWTRQAPGKLEWVGSIINNGSTGY 61
DB 20 EVOLVSGGAVPVGSLRLSCASGFTPDYKSWTRQAPGKLEWVGSIINNGSTGY 79
QY 62 ADVKGRFTSRDANKSLYLQNSLRAEPTAVYCARBAPV-----IMGOG 109
DB 80 ADVKGRFTSRDANKSLYLQNSLRAEPTAVYCARBAPV-----IMGOG 139
QY 110 TLVTSRGGGSGGSGGSSSELTPDPAVSVALGQVTRITCCDSIRSYASYAQQKPGQAP 162
DB 140 TLVTSRGGGSGGSGGSSSELTPDPAVSVALGQVTRITCCDSIRSYASYAQQKPGQAP 176
QY 163 SWYQKRP-----QAPVLYYGNRRPSGIPDRFGSSGNTASLTITGAQ 208
DB 177 -FFQEBLVTWESGCG-----VTARNPSS-----QASGDLVTTSSQLTIPATQ 222

RESULT 15
Q6WU38

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 147.14 Seconds
(without alignments)
630.846 Million cell updates/sec

Title: US-10-029-926D-235

Perfect score: 1266
Sequence: 1 MAEVQLVESGGGVVPRPGSL.....RDSGNHVVFGGKTLTVLG 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1266	100.0	266	5	ABG92020 Human ant
2	1266	100.0	277	5	Abg78150 Human Fv
3	1266	100.0	277	5	ABG91841 Human ant
4	1262	99.7	277	8	Ad128366 Human scf
5	1257	99.3	246	5	ABG78329 Human Fv
6	1257	99.3	246	5	ABG92026 Antibody
7	1250	98.7	256	5	ABG78334 Human Fv
8	1250	98.7	256	5	ABG92025 Antibody
9	1242	98.1	277	5	ABG78328 Human Fv
10	1242	98.1	277	5	ABG92019 Human ant
11	1223.5	96.6	278	8	Ad128367 Human scf
12	1219.5	96.3	280	8	ADJ57363 P-select
13	1218.5	96.2	239	5	ABP44926 Human Bly
14	1218.5	96.2	239	7	ADG95753 Single ch
15	1212.5	95.8	239	7	ABP46027 Human Bly
16	1212.5	95.8	239	7	ADG96854 Single ch
17	1212.5	95.8	239	8	Ad128368 Human scf
18	1191.5	94.1	239	5	ABP46004 Human Bly
19	1191.5	94.1	239	7	ADG96831 Single ch
20	1187	93.8	309	2	AAW83322 Single ch
21	1187	93.8	309	5	ABB09603 Antio ac1
22	1187	93.8	309	6	ABG74384 Single ch
23	1187	93.8	309	7	ADG98737 Human sin
24	1187	93.8	309	8	AD040446 Human sin
25	1181	93.3	238	3	AAV95198 Anti-Plat

26	1178	93.0	244	6	AAO31136 Human CMO
27	1152.5	91.0	260	5	ABG92023 Antibody
28	1149	90.8	242	8	AD158068 Reg IV-sp
29	1144	90.4	263	5	ABG92024 Antibody
30	1139.5	90.0	239	5	ABP46007 Human Bly
31	1139.5	90.0	239	7	ADG96834 Single ch
32	1133	89.5	244	6	AAO31139 Human CMO
33	1132.5	89.5	239	5	ABP46024 Human Bly
34	1132.5	89.5	239	7	ADG96851 Single ch
35	1131.5	89.4	245	6	AAO31137 Human CMO
36	1131	89.3	252	5	ABP45405 Human Bly
37	1131	89.3	252	7	ADG96232 Single ch
38	1129.5	89.2	243	7	ADG30436 Human GMB
39	1127.5	89.1	243	5	ABP46045 Human Bly
40	1127.5	89.1	243	7	ADG96872 Single ch
41	1126.5	89.0	239	5	ABP46012 Human Bly
42	1126.5	89.0	239	7	ADG96839 Single ch
43	1121	88.5	242	7	ADG30497 Human GMC
44	1120	88.5	291	8	ADN06989 Human EPG
45	1119	88.4	240	5	ABP46002 Human Bly

ALIGNMENTS

RESULT 1	ABG92020	standard; protein; 266 AA.
ID	ABG92020	standard; protein; 266 AA.
AC	ABG92020;	
XX		
DT	04-DEC-2002	(first entry)
XX		
DE	Human antibody fragment #204.	
XX		
KM	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;	
KM	metastasis; hypervariable region; autoimmune disease; thrombosis;	
KM	restenosis; leukaemia; inflammatory disease; cardiovascular disease;	
KM	myocardial infarction; retinopathic disease; abnormal platelet function;	
KM	sulphated tyrosine-dependent protein-protein interaction.	
OS	Homo sapiens.	
XX		
PN	WO200253700-A2.	
XX		
PD	11-JUL-2002.	
XX		
PF	31-DEC-2001; 2001WO-US049442.	
XX		
PR	29-DEC-2000; 2000US-00751181.	
PR	29-DEC-2000; 2000US-0258948P.	
XX		
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
XX		
PI	Lazarovits J, Hagai Y, Plaksin P, Vogel T, Nimrod A, Mar-Haim H;	
PI	Seatonch E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;	
XX		
DR	WPI; 2002-674776/72.	
XX		
PT	Novel isolated epitope present on cancer cells and important in	
PT	physiological phenomena such as cell rolling, metastasis and	
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular	
PT	diseases, and cancer.	
XX		
PS	Disclosure; Page 309-310; Opp; English.	
XX		
CC	The invention relates to an isolated epitope present on cancer cells and	
CC	important in physiological phenomena such as cell rolling, metastasis and	
CC	inflammation, where the epitope is capable of being bound by an antibody,	
CC	its antigen-binding fragment or its complex comprising at least one	
CC	antibody or its binding fragment having a first hypervariable region. The	
CC	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune	
CC	disease, thrombosis, restenosis, metastasis, growth and/or replication of	

CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 CC

CC Sequence 266 AA;

Query Match 100.0%; Score 1266; DB 5; Length 266;
 Best Local Similarity 100.0%; Pred. No. 9.1e-81;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVVRRPGSSLRISCAAGTFDDYGMWVQAPGKLEWVSGINWNGST 60
 DB 21 MAEVLVESGGGVVRRPGSSLRISCAAGTFDDYGMWVQAPGKLEWVSGINWNGST 80
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 120
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 140
 QY 121 GSGGGSGGGGSSSELTDPAVSVVALGQTVRITCGDLSRSYSVSWYQKFGQAPVLYYG 180
 DB 141 GSGGGSGGGGSSSELTDPAVSVVALGQTVRITCGDLSRSYSVSWYQKFGQAPVLYYG 200
 QY 181 KNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260

RESULT 2

ABG78150 standard; protein; 277 AA.

XX ABG78150;
 AC
 XX
 DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;
 KM disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

XX WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;

XX DR WPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

XX Claim 4; Page 155-156; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scfv) or a disulfide Fv (dsfv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 CC

XX Sequence 277 AA;

Query Match 100.0%; Score 1266; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 9.5e-81;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVVRRPGSSLRISCAAGTFDDYGMWVQAPGKLEWVSGINWNGST 60
 DB 21 MAEVLVESGGGVVRRPGSSLRISCAAGTFDDYGMWVQAPGKLEWVSGINWNGST 80
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 120
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 140
 QY 121 GSGGGSGGGGSSSELTDPAVSVVALGQTVRITCGDLSRSYSVSWYQKFGQAPVLYYG 180
 DB 141 GSGGGSGGGGSSSELTDPAVSVVALGQTVRITCGDLSRSYSVSWYQKFGQAPVLYYG 200
 QY 181 KNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGMTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260

RESULT 3

ABG91841 standard; protein; 277 AA.

XX ABG91841;

AC ABG91841;
 XX
 DT 04-DEC-2002 (first entry)

DE Human antibody fragment #25.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune diseases; thrombosis;
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

XX DR Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

XX WPI; 2002-674776/72.
DR Novel isolated epitope present on cancer cells and important in
XX physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
XX Claim 23; Page 233-234; Opp; English.
PS
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC restenosis, thrombosis and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
XX Sequence 277 AA;
SO
Query Match 100.0%; Score 1266; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 9, 5e-81;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEVLVESGGGVVPRGGSRLSCAAGFTFDYGMKSWVQAQPKGLEWVSGINMNGST 60
DB 21 MAEVLVESGGGVVPRGGSRLSCAAGFTFDYGMKSWVQAQPKGLEWVSGINMNGST 80
QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYYCARMRAPIVWGQGLTVTSRGGG 120
DB 81 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYYCARMRAPIVWGQGLTVTSRGGG 140
QY 121 GSGGGSGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 180
DB 141 GSGGGSGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 200
QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFVGGGKLTVLG 240
DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFVGGGKLTVLG 260
RESULT 4
ADI28366 standard; protein; 277 AA.
ID ADI28366
XX ADI28366;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human scFv fragment Y1, binds to platelets.
DE
XX Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
KM
XX Homo sapiens.
OS
XX WO2004002528-A1.
XX PN
XX 08-JAN-2004.
XX PD
XX

PF 30-JUN-2003; 2003MO-US020604.
XX
XX 01-JUL-2002; 2002US-00189025.
XX
XX (SAVI-) SAVIENT PHARM INC.
PA
XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
PI
XX WPI; 2004-099189/10.
DR
XX
XX Composition comprising an agent and/or antibody or its fragment, useful
PT for treating autoimmune disease, thrombosis, restenosis, metastasis, or
PT for inhibiting growth and/or replication of tumor cells or leukemia
PT cells.
XX
PS Claim 13; SEQ ID NO 1; 56pp; English.
PS
XX The present sequence is the protein sequence of human scFv fragment Y1.
CC This antibody was identified by screening a human antibody phage library
CC that has diversity only in the heavy chain CDR3 regions. Fixed human
CC platelets were screened in order to identify antibodies that bind
CC platelets. The epitope for Y1 antibody is located between amino acids 272
CC and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the
CC N-terminal of PSGL-1, a receptor for E-, L- and P-selectins, and has a
CC high affinity for primary leukaemia cells. The invention relates to
CC compositions utilising an agent and an antibody or its fragment. The
CC agent is a toxin, radioisotope or pharmaceutical agent such as
CC doxorubicin. It is complexed or combined with or conjugated to the
CC antibody or its fragment. The agent and/or antibody can be present in the
CC composition is a sub-clinical amount, i.e. less than the amount generally
CC found to be clinically effective when the agent is administered alone.
CC The composition is used in claimed methods of: inhibiting cell rolling,
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC replication of tumour cells or leukaemia cells, an increase in number of
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet complex formation, aggregation or
CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
CC susceptibility of disease cells to damage by anti-disease agents, and the
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
CC agents; and ameliorating the effects of a disease, preventing a disease,
CC treating a disease or inhibiting the progress of a disease.
XX
XX Sequence 277 AA;
SO
Query Match 99.7%; Score 1262; DB 8; Length 277;
Best Local Similarity 99.6%; Pred. No. 1, 8e-80;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEVLVESGGGVVPRGGSRLSCAAGFTFDYGMKSWVQAQPKGLEWVSGINMNGST 60
DB 21 MAEVLVESGGGVVPRGGSRLSCAAGFTFDYGMKSWVQAQPKGLEWVSGINMNGST 80
QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYYCARMRAPIVWGQGLTVTSRGGG 120
DB 81 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYYCARMRAPIVWGQGLTVTSRGGG 140
QY 121 GSGGGSGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 180
DB 141 GSGGGSGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 200
QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFVGGGKLTVLG 240
DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFVGGGKLTVLG 260
RESULT 5
ABG78329 standard; protein; 246 AA.
ID ABG78329
XX ABG78329;
AC
XX 15-NOV-2002 (first entry)
DT
XX

DE Human Fv molecule hypervariable region related peptide #204.
 XX
 XX Human: Fv molecule; hypervariable region; single chain Fv; cytosolic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIO-T) BIO-TECHNOLOGY GEN CORP.
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A,
 PI Plakain D, Peretz T;
 DR MPI; 2002-619166/66.
 XX
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 XX Disclosure; Page 44-45; 232pp; English.
 XX
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 CC
 XX
 SQ Sequence 246 AA;
 Query Match 99.3%; Score 1257; DB 5; Length 246;
 Best Local Similarity 100.0%; Pred. No. 3.6e-80;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTWRQAPGKLEWVSGINNNGSGTGY 62
 DB 2 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTWRQAPGKLEWVSGINNNGSGTGY 61
 QY 63 ADSVKGRFTISRDAKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 122
 DB 62 ADSVKGRFTISRDAKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 121
 QY 123 GGGGSGGGGSELTPDPAVSVALGQTVRITCGDLSLSYASWYQOKPGQAPVLVIYGN 182
 DB 122 GGGGSGGGGSELTPDPAVSVALGQTVRITCGDLSLSYASWYQOKPGQAPVLVIYGN 181
 QY 183 NRPSGIDPRFSGSSSGNTASITITGAQADEADYYCNSRDSSGNHVVFGGGTKLTVLG 240
 DB 182 NRPSGIDPRFSGSSSGNTASITITGAQADEADYYCNSRDSSGNHVVFGGGTKLTVLG 239
 RESULT 6
 ABG92026
 ID ABG92026 standard; protein; 246 AA.
 XX

AC ABG92026;
 XX
 XX 04-DEC-2002 (first entry)
 DT
 XX
 DE Antibody protein #5.
 XX
 XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM reneosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Unidentified.
 XX
 PN MO200253700-A2.
 XX
 PD 11-UTL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIO-T) BIO-TECHNOLOGY GEN CORP.
 PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H,
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 DR MPI; 2002-674776/72.
 XX
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 XX Disclosure; Fig 52; 0pp; English.
 XX
 XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, reneosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 CC
 XX
 SQ Sequence 246 AA;
 Query Match 99.3%; Score 1257; DB 5; Length 246;
 Best Local Similarity 100.0%; Pred. No. 3.6e-80;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTWRQAPGKLEWVSGINNNGSGTGY 62
 DB 2 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTWRQAPGKLEWVSGINNNGSGTGY 61
 QY 63 ADSVKGRFTISRDAKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 122
 DB 62 ADSVKGRFTISRDAKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 121

QY 123 GGGGSGGGSSSELTQDPVAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 182
 DB 122 GGGGSGGGSSSELTQDPVAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 181
 QY 183 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 240
 DB 182 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 239

RESULT 7
 ABG78334
 ID ABG78334 standard; protein; 256 AA.
 AC ABG78334;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #209.
 XX
 KM Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KM disulfide Fv; dafv, gcfv; cancer; carcinoma; sarcoma; leukemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200259264-A2.
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX
 DR WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 or fragment, or construct of fragment with enhanced binding
 characteristics so as to selectively bind target cell in favor of other
 cells.

Example 9; Page 90; 232pp; English.

The invention relates to a peptide or polypeptide comprising an Fv
 molecule, a construct or fragments or a construct of a fragment with
 enhanced binding characteristics which selectively and/or specifically
 binds to a target cell in favour of other cells, where binding is
 primarily determined by a first hypervariable region and Fv is a single
 chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 association with or attached, coupled, combined, linked or fused to a
 pharmaceutical agent, is useful in the manufacture of a medicament, where
 the medicament has activity against a diseased cell, preferably a cancer
 cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
 myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
 acute myeloid leukemia cell). The peptide is also useful for preparing a
 composition for use in inhibiting the growth of a diseased or cancer
 cell. This sequence represents a human Fv molecule hypervariable region
 related peptide of the invention

Sequence 256 AA;
 SQ

Query Match 98.7%; Score 1250; DB 5; Length 256;
 Best Local Similarity 99.6%; Pred. No. 1.2e-79;
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EVOLVBSGGGVNPPGSGSLRLSCAASGFTFDYGMWVRQAPGKGLEWVSGINNNGSGTGY 62
 DB 2 EVOLVBSGGGVNPPGSGSLRLSCAASGFTFDYGMWVRQAPGKGLEWVSGINNNGSGTGY 61

QY 63 ADSVKRFTISRDNANSLYLQNNSLRAEDTAVYCARMPAPYIWOGTLTVTSRGGGGS 122
 DB 62 ADSVKRFTISRDNANSLYLQNNSLRAEDTAVYCARMPAPYIWOGTLTVTSRGGGGS 121
 QY 123 GGGGSGGGSSSELTQDPVAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 182
 DB 122 GGGGSGGGSSSELTQDPVAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 181
 QY 183 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 240
 DB 182 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 239

RESULT 8
 ABG92025
 ID ABG92025 standard; protein; 256 AA.
 AC ABG92025;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Antibody biotag #1.
 XX
 KM Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM restenosis; leukemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Unidentified.
 XX
 PN WO200253700-A2.
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Stanton E, Richter T, Amit B, Koepelman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.

Novel isolated epitope present on cancer cells and important in
 physiological phenomena such as cell rolling, metastasis and
 inflammation, for treating autoimmune, inflammatory or cardiovascular
 diseases, and cancer.

Disclosure; Fig 51; Opp; English.

The invention relates to an isolated epitope present on cancer cells and
 important in physiological phenomena such as cell rolling, metastasis and
 inflammation, where the epitope is capable of being bound by an antibody,
 its antigen-binding fragment or its complex comprising at least one
 antibody or its binding fragment having a first hypervariable region. The
 epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 disease, thrombosis, restenosis, metastasis, growth and/or replication of
 tumour or leukemia cells, increase in number of tumour or leukemia
 cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 platelet and/or cell-platelet adhesion or aggregation, for increasing
 mortality of tumour or leukemia cells, for increasing the susceptibility
 of diseased cells to damage by anti-disease, anti-cancer or anti-
 leukemia agents, or for decreasing the number of tumour or leukemia
 cells in a patient, or in the manufacture of a medicament for the above
 mentioned purposes. The epitopes are useful for diagnosing and treating
 diseases such as cancer, leukemia, autoimmune diseases, inflammatory
 diseases, cardiovascular diseases such as myocardial infarction,
 retinopathic diseases and other diseases mediated by abnormal platelet
 function and diseases caused by sulphated tyrosine-dependent protein-

CC protein interactions. This sequence represents an antibody biotag used in
 CC the scope of the invention
 XX
 SQ Sequence 256 AA;

Query Match 98.7%; Score 1250; DB 5; Length 256;
 Best Local Similarity 99.6%; Pred. No. 1.2e-79;
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EVLVVSSGGVVRPGSLRLSCAASGTPPDYGMVSRQAPGKLEWVSGINMGSTG 62
 DB 2 EVLVVSSGGVVRPGSLRLSCAASGTPPDYGMVSRQAPGKLEWVSGINMGSTG 61
 QY 63 ADVKGRFTISRDNKAKSLYLQNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGG 122
 DB 62 ADVKGRFTISRDNKAKSLYLQNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGG 121
 QY 123 GGGGSGGGGSELTPDPVAVSVALGQTVRITCGDLSRYASWYQKPGQAPVLIYGN 182
 DB 122 GGGGSGGGGSELTPDPVAVSVALGQTVRITCGDLSRYASWYQKPGQAPVLIYGN 181
 QY 183 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGTKLTVLG 240
 DB 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGTKLTVLG 239

RESULT 9
 ABG78328 standard; protein; 277 AA.
 ID ABG78328
 AC ABG78328;
 XX
 DT 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #203.
 DE
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.
 OS
 PN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarevits J, Guy R, Lipschitz O, Stanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX
 DR WPI; 2002-619166/66.
 DR N-PSDB; ABS63384.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

PS Claim 141; Fig 14; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX

SQ Sequence 277 AA;
 Query Match 98.1%; Score 1242; DB 5; Length 277;
 Best Local Similarity 97.9%; Pred. No. 4.5e-79;
 Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVSSGGVVRPGSLRLSCAASGTPPDYGMVSRQAPGKLEWVSGINMGSTG 60
 DB 21 MAEVLVSSGGVVRPGSLRLSCAASGTPPDYGMVSRQAPGKLEWVSGINMGSTG 80
 QY 61 GVADSVKGRFTISRDNKAKSLYLQNSLRAEDTAVYYCARLTHPYFMGGTLVTVSRGGG 120
 DB 81 GVADSVKGRFTISRDNKAKSLYLQNSLRAEDTAVYYCARLTHPYFMGGTLVTVSRGGG 140
 QY 121 GSGGGSGGGGSELTPDPVAVSVALGQTVRITCGDLSRYASWYQKPGQAPVLIYGN 180
 DB 141 GSGGGSGGGGSELTPDPVAVSVALGQTVRITCGDLSRYASWYQKPGQAPVLIYGN 200
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGTKLTVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGTKLTVLG 260

RESULT 10
 ABG92019 standard; protein; 277 AA.
 ID ABG92019
 AC ABG92019;
 XX
 DT 04-DEC-2002 (first entry)

XX Human antibody fragment #203.
 DE
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.
 OS
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Stanton E, Richter T, Amit B, Koepman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

PS Claim 23; Page 308-309; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and

CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 CC
 CC

XX Sequence 277 AA;

Query Match 98.1%; Score 1242; DB 5; Length 277;
 Best Local Similarity 97.9%; Pred. No. 4.5e-79;
 Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSRLSCAASGFFPDYGMISWVROAPGKLEWVSGINNGGST 60
 DB 21 MAEVLVESGGGVRRPGSRLSCAASGFFPDYGMISWVROAPGKLEWVSGINNGGST 80
 QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARMAPVIMGGTILVTVSRGG 120
 DB 81 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARMAPVIMGGTILVTVSRGG 140
 QY 121 GSGGGSGGGGSSSLTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIYG 180
 DB 141 GSGGGSGGGGSSSLTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIYG 200
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 240
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 260

RESULT 11

ID ADI28367 standard; protein; 278 AA.

XX AC ADI28367;

DT 06-MAY-2004 (first entry)

XX DE Human scFv fragment Y17, binds to platelets.

XX KM Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

XX OS Homo sapiens.

XX PN WO2004002528-A1.

XX PD 08-JAN-2004.

XX PF 30-JUN-2003; 2003WO-US020604.

XX PR 01-JUL-2002; 2002US-00189025.

XX PA (SAVI-) SAVIENT PHARM INC.

XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

XX DR WPI; 2004-099189/10.

XX PT Composition comprising an agent and/or antibody or its fragment, useful

PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 PT for inhibiting growth and/or replication of tumor cells or leukemia
 PT cells.

XX Claim 13; SEQ ID NO 2; 58pp; English.

XX PS The present sequence is the protein sequence of human scFv fragment Y17.
 CC This antibody was identified by screening a human antibody phage library
 CC that has diversity only in the heavy chain CDR3 regions. Fixed human
 CC platelets were screened in order to identify antibodies that bind
 CC platelets. Y17 binds leukaemic cells. The invention relates to
 CC compositions utilising an agent and an antibody or its fragment. The
 CC agent is a toxin, radioisotope or pharmaceutical agent such as
 CC doxorubicin. It is complexed or combined with or conjugated to the
 CC antibody or its fragment. The agent and/or antibody can be present in the
 CC composition in a sub-clinical amount, i.e. less than the amount generally
 CC found to be clinically effective when the agent is administered alone.
 CC The composition is used in claimed methods of: inhibiting cell rolling,
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
 CC replication of tumour cells or leukaemia cells, an increase in number of
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
 CC susceptibility of disease cells to damage by anti-disease agents, and the
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
 CC agents; and ameliorating the effects of a disease, preventing a disease,
 CC treating a disease or inhibiting the progress of a disease.

XX SQ Sequence 278 AA;

Query Match 96.6%; Score 1223.5; DB 8; Length 278;
 Best Local Similarity 97.5%; Pred. No. 9e-78;
 Matches 235; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAEVLVESGGGVRRPGSRLSCAASGFFPD-DYGMISWVROAPGKLEWVSGINNGGS 59
 DB 21 MAEVLVESGGGVRRPGSRLSCAASGFFPDTHFYFWROAPGKLEWVSGINNGGS 80
 QY 60 TGYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARMAPVIMGGTILVTVSRGG 119
 DB 81 TGYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARMAPVIMGGTILVTVSRGG 140
 QY 120 GSGGGSGGGGSSSLTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIY 179
 DB 141 GSGGGSGGGGSSSLTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIY 200
 QY 180 GKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 239
 DB 201 GKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 260
 QY 240 G 240
 DB 261 G 261

RESULT 12

ID ADJ57363 standard; protein; 280 AA.

XX AC ADJ57363;

DT 06-MAY-2004 (first entry)

XX DE P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32.

XX KM P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;

XX KW antiinflammatory; immunosuppressive; human.

XX OS Homo sapiens.

XX XX Key Location/Qualifiers

XX FT 53..60 Region /label= CDR1

FT /note= "Specifically referred to in Claim 2"
 FT 75. .90
 FT /label= CDR2
 FT /note= "Specifically referred to in Claim 2"
 FT 124. 129
 FT /label= CDR3
 FT /note= "Specifically referred to in Claim 2"
 XX
 XX WO2004003166-A2.
 XX
 XX 08-JAN-2004.
 XX
 XX 30-JUN-2003; 2003WO-US020602.
 XX
 XX 01-JUL-2002; 2002US-00189032.
 XX
 XX (SAVI-) SAVIENT PHARM INC.
 XX
 XX Levanon A, Ben-Levy R, Plaksin D, Stanton E, Hagai Y,
 XX Hoch Mar- Chaim H;
 XX
 XX WPI; 2004-203378/19.
 XX
 XX Novel antibody or its fragment that binds to an epitope of P-Selectin-
 PT Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,
 PT infection, auto-immune disease, metastasis, tumor/leukemia cell in
 PT patient.
 XX
 XX Claim 1; SEQ ID NO 1; 106pp; English.
 XX
 XX The present sequence is that of an scFv antibody fragment, designated
 CC L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody
 CC was identified by screening a phage library, which had diversity only in
 CC the heavy chain CDR3 regions, against a leukemia cell to select specific
 CC antibodies that recognised leukemia cell surface determinants, wherein
 CC the specific receptor was not previously known or characterised. The
 CC invention relates to an antibody or its fragment having the binding
 CC capabilities of L32. Such antibodies can be used in therapeutic,
 CC diagnostic, prognostic and staging methods. Pharmaceutical compositions
 CC comprising such antibodies are used to treat conditions related to:
 CC inhibiting or treating cell rolling, inflammation, autoimmune disease,
 CC infection (e.g. HIV infection), metastasis, and growth and/or replication
 CC of tumour cells; increasing the mortality of tumour cells; inhibiting
 CC growth and/or replication of tumour cells; inhibiting growth and/or
 CC replication of leukaemia cells; increasing the mortality rate of
 CC leukaemia cells; altering the susceptibility of diseased cells to damage
 CC by anti-disease agents; increasing the susceptibility of tumour cells to
 CC damage by anti-cancer agents; increasing the susceptibility of leukaemia
 CC cells to damage by anti-leukaemia agents; inhibiting increase in number
 CC of tumour cells in a patient; decreasing the number of tumour cells in a
 CC patient; inhibiting increase in number of leukaemia cells in a patient;
 CC and decreasing the number of leukaemic cells in a patient. Other methods
 CC are provided to induce antibody-dependent cell-mediated cytotoxicity or
 CC stimulate natural killer or T cells using the antibodies. A method of
 CC purging tumour cells from a patient involves incubating the cells with
 CC the antibody.
 CC
 XX
 XX Sequence 280 AA:
 SQ
 Query Match 96.3%; Score 1219.5; DB 8; Length 280;
 Best Local Similarity 96.7%; Pred. No. 1.7e-77;
 Matches 235; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
 QY 1 MAEVLVESGGGVPRGSLRLCSAASGFTD---DYGMSVVRAPKGLIEWSGINWG 57
 DB 21 MAEVLVESGGGVPRGSLRLCSAASGFTDLPKVMKVVRAAPGKLEWWSGINWG 80
 QY 58 GSTVAASVYKGRFTISRDNANKNSLYLQNNISRAEDTAVVYCARARAVINWGQTLTVVSR 117
 DB 81 GSTVAASVYKGRFTISRDNANKNSLYLQNNISRAEDTAVVYCARARAVINWGQTLTVVSR 140
 QY 118 GGGSGGGGGGGSSSELTQDPAVSVALGQTVRITTCGDSIRSYASWYQKPGQAPFLV 177

DB 141 GGGSGGGGGGGSSSELTQDPAVSVALGQTVRITTCGDSIRSYASWYQKPGQAPFLV 200
 QY 178 IYKKNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYCNRSDDSGNHHVFGGTXLT 237
 DB 201 IYKKNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYCNRSDDSGNHHVFGGTXLT 260
 QY 238 VLQ 240
 DB 261 VLQ 263
 RESULT 13
 ABP44926
 ID ABP44926 standard; protein, 239 AA.
 XX
 XX ABP44926;
 XX
 XX 19-AUG-2002 (first entry)
 XX
 XX Human BlyS binding scFv SEQ ID 937.
 DE
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US019110.
 XX
 XX 16-JUN-2000; 2000US-0212210P.
 XX 17-OCT-2000; 2000US-0240816P.
 XX 16-MAR-2001; 2001US-0276248P.
 XX 21-MAR-2001; 2001US-0277379P.
 XX 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 XX WPI; 2002-114799/15.
 XX
 XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 1520-1521; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 XX Sequence 239 AA:
 SQ

Query Match 96.2%; Score 1218.5; DB 5; Length 239;
 Best Local Similarity 97.9%; Pred. No. 1.7e-77;
 Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVAPPGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 62
 DB 1 EVOLVESGGGVAPPGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 60
 QY 63 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 121
 DB 61 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120
 QY 122 SGGSGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLYYTK 181
 DB 121 SGGSGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLYYTK 180
 QY 182 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGSHVVFSGGTRLTVLG 240
 DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGSHVVFSGGTRLTVLG 239

RESULT 14
 ID ADG95753 standard; protein; 239 AA.
 XX ADG95753;

DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds Blys SeqID 937.

KM antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
 KW antiinflammatory; antiaesthetic; antiallergic; cytostatic.

XX Unidentified.

OS WO2003055979-A2.

PN 10-JUL-2003.

PD 14-NOV-2002; 2002WO-US036496.

PF 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

PI WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator

PT (Blys), useful for detecting and treating diseases or disorders e.g.

XX rheumatoid arthritis, asthma and leukemia.

PT Example 1; SEQ ID NO 937; 394bp; English.

XX This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders

CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiallergic, neuroprotective,
 CC antiinflammatory, antiaesthetic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIFO at fcp.wifo.at/pub/published pct_sequences.

QY Sequence 239 AA;
 XX
 Query Match 96.2%; Score 1218.5; DB 7; Length 239;
 Best Local Similarity 97.9%; Pred. No. 1.7e-77;
 Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVAPPGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 62
 DB 1 EVOLVESGGGVAPPGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 60
 QY 63 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 121
 DB 61 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120
 QY 122 SGGSGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLYYTK 181
 DB 121 SGGSGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLYYTK 180
 QY 182 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGSHVVFSGGTRLTVLG 240
 DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGSHVVFSGGTRLTVLG 239

RESULT 15
 ID ABP46027 standard; protein; 239 AA.
 XX ABP46027;

AC ABP46027;

DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 2038.

DE Human Blys binding scFv SEQ ID 2038.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

PN 10-JAN-2002.

PD 15-JUN-2001; 2001WO-US019110.

PF 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX
PS Claim 1; Page 2830-2831; 3148pp; English.

XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antithumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

SO Sequence 239 AA;

Query Match 95.8%; Score 1212.5; DB 5; Length 239;

Best Local Similarity 97.5%; Pred. No. 4.5e-77;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 3 EYQLVSSGGGVPRPGSLRLSCAASGTFPDYGMWVRQAPGKLEWVSGINMGSTGY 62
DB 1 EYQLVSSGGGVPRPGSLRLSCAASGTFPDYGMWVRQAPGKLEWVSGINMGSTGY 60
QY 63 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKMR-APVWGQGLTVTSRGGG 121
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRRYALDYWGQGLTVTSRGGG 120
QY 122 SGGGSSGGGSSSLTQDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGR 181
DB 121 SGGGSSGGGSSSLTQDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGR 180
QY 182 NNRPSGIPDRFSSSSSGNTASLTITGAQADEADYYCNSRDSGNTVYRGGGTKLTVLG 240
DB 181 NNRPSGIPDRFSSSSSGNTASLTITGAQADEADYYCNSRDSGNTVYRGGGTKLTVLG 239

Search completed: April 25, 2005, 20:22:31
Job time : 148.14 secs

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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 36.9845 Seconds
(without alignments)
484.413 Million cell updates/sec

Title: US-10-029-926D-235

Perfect score: 1266
Sequence: 1 MAEVLVSGGGVRRPGSL.....RDSGNHVFGGKTLVLG 240

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfilist.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1187	93.8	309	3	US-09-079-029-9
2	1105.5	87.3	312	3	US-09-079-029-10
3	1104.5	87.2	280	3	US-09-260-527-1
4	952.5	75.2	278	3	US-09-260-527-3
5	884.5	69.9	310	3	US-09-079-029-11
6	822	64.9	268	4	US-09-976-118-1
7	803	63.4	240	4	US-09-192-854-2
8	791.5	62.5	334	4	US-09-646-028-53
9	791.5	62.5	339	4	US-09-646-028-55
10	791.5	62.5	348	4	US-09-646-028-51
11	783.5	61.9	245	3	US-08-918-148-75
12	780.5	61.7	245	4	US-09-138-091A-73
13	780.5	61.7	245	4	US-08-918-148-76
14	780.5	61.7	245	4	US-09-138-091A-74
15	777.5	61.4	245	4	US-08-918-148-78
16	777.5	61.4	245	4	US-09-138-091A-76
17	756.5	59.8	281	3	US-09-025-769B-178
18	756.5	59.8	281	4	US-09-490-070A-178
19	756.5	59.8	281	4	US-09-490-153-178
20	756.5	59.8	281	4	US-09-490-324-178
21	753	59.5	244	4	US-08-918-148-77
22	753	59.5	244	4	US-09-138-091A-75
23	726.5	57.4	240	1	US-08-488-113B-148
24	726.5	57.4	240	1	US-08-477-484B-148
25	726.5	57.4	240	2	US-08-646-360-148
26	726.5	57.4	240	3	US-08-839-765-148
27	726.5	57.4	240	3	US-09-136-389-148

28	726.5	57.4	240	3	US-09-610-838-148	Sequence 148, App
29	726.5	57.4	240	4	US-09-711-485-148	Sequence 148, App
30	712.5	56.3	284	3	US-08-564-164A-2	Sequence 2, App1
31	711	56.2	255	3	US-09-553-498-8	Sequence 8, App1
32	711	56.2	255	4	US-09-618-869-8	Sequence 8, App1
33	710	56.1	244	3	US-08-918-148-79	Sequence 79, App1
34	710	56.1	244	4	US-09-138-091A-77	Sequence 77, App1
35	709.5	56.0	289	3	US-09-184-658-63	Sequence 63, App1
36	709.5	56.0	289	4	US-09-504-262D-63	Sequence 63, App1
37	708	55.9	301	2	US-08-661-052-14	Sequence 14, App1
38	708	55.9	301	3	US-09-188-082-14	Sequence 14, App1
39	708	55.9	301	3	US-09-364-088-14	Sequence 14, App1
40	708	55.9	301	3	US-09-102-716-14	Sequence 14, App1
41	708	55.9	553	2	US-08-661-052-16	Sequence 16, App1
42	708	55.9	553	3	US-09-188-082-16	Sequence 16, App1
43	708	55.9	553	3	US-09-364-088-16	Sequence 16, App1
44	708	55.9	553	3	US-09-102-716-16	Sequence 16, App1
45	707	55.8	236	2	US-08-190-199A-65	Sequence 65, App1

ALIGNMENTS

```
RESULT 1
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
;
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatcin (Genentech)
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9681
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-079-029-9
;
Query Match 93.8%; Score 1187; DB 3; Length 309;
Best Local Similarity 92.3%; Pred. No. 1.2e-88;
Matches 227; Conservative 5; Mismatches 8; Indels 6; Gaps 1;
```

QY 1 MAEVLVSGGGVRRPGSLIRLSCASGTFPDYIGMSWVRQAFGKLEWVSGINNNGSST 60
DB 38 MAEVLVSGGGVRRPGSLIRLSCASGTFPDYIGMSWVRQAFGKLEWVSGINNNGSST 97
QY 61 GYADVSKGRFTISRDAKNSLYIQNWSLRADPTAVVYCARMRAP-----VINGGCTLVLT 114

```

Db      98  GYADSVKGRVTITISRDNAKNSLYIQMNSLRADPTAVVYCAKILGAGRGWYFDLWGKGTWY 157
QY      115  VSSGGGGGGGGGGGGSSSELTODPAVSVALGOTVITTCQDLSRYSYASWYQKGOAP 174
Db      158  VSSGGGGGGGGGGGGSSSELTODPAVSVALGOTVITTCQDLSRYSYASWYQKGOAP 217
QY      175  VLVIYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEGGT 234
Db      218  VLVIYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEGGT 277
QY      235  KLTVLG 240
Db      278  KLTVLG 283

```

RESULT 2

```

US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntatapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Minipat (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-10

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Query Match 87.3%; Score 1105.5; DB 3; Length 312;

Best Local Similarity 86.7%; Pred. No. 4.9e-82; Indels 9; Gaps 1;

```

Matches 216; Conservative 5; Mismatches 19; Indels 9; Gaps 1;
QY      1  MAEQVLVESGGGVRRPGGSLRLSCAASGFTFDYDGMGSMWRQAPGKGLEWYSGINWNGSGT 60
Db      38  MAGQVLVESGGGLVQPGSLRLSCAASGFTFSSYTMNSWVAQAPGKGLEWVANIKQDSSEK 97
QY      61  GYADSVKGRFTISRDNAKNSLYIQMNSLRADPTAVVYCAKILGAGRGWYFDLWGKGTWY 111
Db      98  YYVDYVKGKRFITISRDNAKNSLYIQMNSLRADPTAVVYCAKILGAGRGWYFDLWGKGTWY 157
QY      112  LNVYSRGGGGGGGGGGSSSELTODPAVSVALGOTVITTCQDLSRYSYASWYQKGOAP 171
Db      158  TVIVSSGGGGGGGGGGSSSELTODPAVSVALGOTVITTCQDLSRYSYASWYQKGOAP 217

```

```

QY      172  QAPVLVIYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEG 231
Db      218  QAPVLVIYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEG 277
QY      232  GGTKLTVLG 240
Db      278  GGTKLTVLG 286

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RESULT 3

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US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic acFv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
; US-09-260-527-1

```

Query Match 87.2%; Score 1104.5; DB 3; Length 280;

Best Local Similarity 86.5%; Pred. No. 5.2e-82; Indels 3; Gaps 2;

Matches 215; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

```

QY      1  MAEQVLVESGGGVRRPGGSLRLSCAASGFTFDYDGMGSMWRQAPGKGLEWYSGI--NMNGG 58
Db      21  MAEQVLVESGGGLVQPGSLRLSCAASGFTFSSYTMNSWVAQAPGKGLEWVANIKQDSSEK 80
QY      59  STGYADSVKGRFTISRDNAKNSLYIQMNSLRADPTAVVYCAKILGAGRGWYFDLWGKGTWY 117
Db      81  TTDYAAPVKGKRFITISRDNAKNSLYIQMNSLRADPTAVVYCAKILGAGRGWYFDLWGKGTWY 140
QY      118  GGGGGGGGGGGGGSSSELTODPAVSVALGOTVITTCQDLSRYSYASWYQKGOAPVLV 177
Db      141  GGGGGGGGGGGGGSSSELTODPAVSVALGOTVITTCQDLSRYSYASWYQKGOAPVLV 200
QY      178  IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEGGT 237
Db      201  IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFEGGT 260
QY      238  VLG 240
Db      261  VLG 263

```

RESULT 4

```

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

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QY 230 FGGGKLTVLG 240
Db 240 FGTGKTVLVG 250

RESULT 7
US-09-192-854-2
Sequence 2, Application US/09192854
Patent No. 6696245
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-2

Query Match 63.4%; Score 803; DB 4; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.2e-57;
Matches 159; Conservative 27; Mismatches 48; Indels 6; Gaps 4;

QY 3 EVOLVESGGGVPRPGSLRLSCAASGFTPDYGMKSWRQAPGKGLEWVSGINMGSTGY 62
1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWRQAPGKGLEWVSAISGSGSTYY 60
Db 63 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRMAPV-IMGQGLTVTVSRGGG 121
61 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKSGYGAFGYWGQGLTVTVSSGGG 120
QY 122 GGGGGGGGGSS--ELTQDP-AVSVVALGQTVRITCGQDSLRSYASWYQKPGQAPLV 178
121 GGGGGGGGGSTDTQMTQSPSSLSASVGDRTYITCRASQSTISYLWYQKPGKAPFL 180
Db 179 YGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGT 238
181 YAASSLQSGVPSRFGSGSGTDFTLTITSSLPEDFAITYYCQQSISTYEN--TFGGTIVEI 238
Db

RESULT 8
US-09-646-028-53
Sequence 53, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 334
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of artificial sequence:/note=synthetic construct
US-09-646-028-53

Query Match 62.5%; Score 791.5; DB 4; Length 334;

Best Local Similarity 64.1%; Pred. No. 1.5e-56;
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

QY 3 EVOLVESGGGVPRPGSLRLSCAASGFTPDYGMKSWRQAPGKGLEWVSGINMGSTGY 62
80 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWRQAPGKGLEWVSAISGSGSTYY 139
Db 63 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRMAPV-IMGQGLTVTVSR 117
140 ADVKGRFASRDNSKNTLYLQNNLRPNDAVYFCANNQTFCLDNWQGLTVTVSSR 199
QY 118 GGGGGGGGGSS--SELTQDP-AVSVVALGQTVRITCGQDSLRSYASWYQKPG 171
200 GGGGGGGGGSGGSGSVLTQPPSVSAAPGQRTVISTGSRNSITGAGYDVWYQKFP 259
Db 172 QAPLVLYYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVF 231
260 TAPKVLISNNRPSGVPRFGSGSGTSASLTITGLQLEDBGTYYCQCNDSLSGWLFG 319
QY 232 GGTGLTVL 239
Db 320 GGTGLTVL 327

RESULT 9
US-09-646-028-55
Sequence 55, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55
LENGTH: 339
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

Query Match 62.5%; Score 791.5; DB 4; Length 339;
Best Local Similarity 64.1%; Pred. No. 1.5e-56;
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

QY 3 EVOLVESGGGVPRPGSLRLSCAASGFTPDYGMKSWRQAPGKGLEWVSGINMGSTGY 62
85 EVOLVESGGGLVPGGSLRLSCAASGFTFSYAMSWRQAPGKGLEWVSAISGSGSTYY 144
Db 63 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRMAPV-IMGQGLTVTVSR 117
145 ADVKGRFASRDNSKNTLYLQNNLRPNDAVYFCANNQTFCLDNWQGLTVTVSSR 204
QY 118 GGGGGGGGGSS--SELTQDP-AVSVVALGQTVRITCGQDSLRSYASWYQKPG 171
205 GGGGGGGGGSGGSGSVLTQPPSVSAAPGQRTVISTGSRNSITGAGYDVWYQKFP 264
Db 172 QAPLVLYYKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVF 231
265 TAPKVLISNNRPSGVPRFGSGSGTSASLTITGLQLEDBGTYYCQCNDSLSGWLFG 324
QY 232 GGTGLTVL 239
Db 325 GGTGLTVL 332


```
RESULT 10
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biregym, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

Query Match          62.5%; Score 791.5; DB 4; Length 348;
Best Local Similarity 64.1%; Pred. No. 1.6e-56;
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

QY 3 EVQLVESGGGVVRPGGSLRLSCAASGFTPDYGMKSWYRQAPGKLEWVSGINMGSGTGY 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   94 EVQLVESGGGVLRISGASGLTFSASITWYRQAPGKLEWVSGISFGDTYY 153
QY 63 ADSVKRFTSRNARKSLYQNMNRLRAEDTAVYYCAKRMARPIY----WGQGLTVY-SR 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   154 ADSVKRFTSRNARKSLYQNMNRLRAEDTAVYYCAKRMARPIY----WGQGLTVYSSR 213
DB 154 ADSVKRFTSRNARKSLYQNMNRLRAEDTAVYYCAKRMARPIY----WGQGLTVYSSR 213
QY 118 GGGSGGGSGGGSGGSS--SETQDPAVSVALGQTVRTTCQDLSLR--SYASWYQOKPG 171
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   214 GGGSGGGSGGGSGGSGSLTLPSPVSALPGQRTVITSCGSSNIGAGIDVWYQKPE 273
DB 214 GGGSGGGSGGGSGGSGSLTLPSPVSALPGQRTVITSCGSSNIGAGIDVWYQKPE 273
QY 172 QAPLVLYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFG 231
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   274 TAPKVLISNNRPSGVDRFSGSKSGTSLAITGLQLEDEGYVYQCNDDSLGLFCG 333
DB 274 TAPKVLISNNRPSGVDRFSGSKSGTSLAITGLQLEDEGYVYQCNDDSLGLFCG 333
QY 232 GGTKLTVL 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 232 GGTKLTVL 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 334 GGTKLTVL 341
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendley, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75

Query Match          61.9%; Score 783.5; DB 3; Length 245;
Best Local Similarity 65.4%; Pred. No. 4.7e-56;
Matches 159; Conservative 28; Mismatches 49; Indels 7; Gaps 4;
```

```
QY 1 MAEVLVESGGGVVRPGGSLRLSCAASGFTPDYGMKSWYRQAPGKLEWVSGINMGSGT 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAEVLVQSGGGLVYKGGSLRLSCAASGFTPSDYMSWIRQAPGKLEWVSYSSSGSTI 60
QY 61 GYADSVKGRFTISRDNARSLYQNMNRLRAEDTAVYYCAKRMAR--APVIMGGTLTVTSR 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GYADSVKGRFTISRDNARSLYQNMNRLRAEDTAVYYCAKRMAR--APVIMGGTLTVTSR 120
QY 118 GGGSGGGSGGGSGGSS--ELTQDPA-VSVALGQTVRTTCQDLSLRSYASWYQOKPGQAPV 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GGGSGGGSGGGSGGSGSLVWYQSPSTLSASVGDVAITTCASSEGIYHMLAWYQOKPGAPK 180
QY 176 LVIYGNRNPSPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGCTK 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 LLIYKASLSLSPASGAPSRFSGSGADFTLTISLQPDPAFYTC--QQYSNYPPLTFGGGCTK 238
QY 236 LTV 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 236 LTV 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 239 LEV 241
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-138-091A-73
; Sequence 73, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendley, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73

Query Match          61.9%; Score 783.5; DB 4; Length 245;
Best Local Similarity 65.4%; Pred. No. 4.7e-56;
Matches 159; Conservative 28; Mismatches 49; Indels 7; Gaps 4;
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Tue Apr 26 17:12:00 2005

us-10-029-926d-235.ral

Page 7

Job time : 37.9845 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 106.164 Seconds
(without alignments)
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Title: US-10-029-926D-235

Perfect score: 1266

Sequence: 1 MAEVLVESGGGVRRPGSL.....RDSGNHVVGSGTKLTIVG 240

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Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Published Applications AA:
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20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1266	100.0	266	US-10-032-037B-204	Sequence 204, App
2	1266	100.0	266	US-10-029-988B-204	Sequence 204, App
3	1266	100.0	266	US-10-032-423A-204	Sequence 204, App
4	1266	100.0	277	US-10-032-037B-25	Sequence 25, App1
5	1266	100.0	277	US-10-029-988B-25	Sequence 25, App1
6	1266	100.0	277	US-10-032-423A-25	Sequence 25, App1
7	1266	100.0	277	US-10-029-926B-25	Sequence 25, App1
8	1242	98.1	277	US-10-032-037B-203	Sequence 203, App
9	1242	98.1	277	US-10-029-988B-203	Sequence 203, App
10	1242	98.1	277	US-10-032-423A-203	Sequence 203, App
11	1242	98.1	277	US-10-029-926B-203	Sequence 203, App
12	1218.5	96.2	239	US-09-880-748-937	Sequence 937, App
13	1218.5	96.2	239	US-10-293-418-937	Sequence 937, App

14	1214.5	95.9	280	US-10-880-922-6	Sequence 6, App1
15	1212.5	95.8	239	US-09-880-748-2038	Sequence 2038, App
16	1212.5	95.8	239	US-10-293-418-2038	Sequence 2038, App
17	1205.5	95.2	280	US-10-880-922-5	Sequence 5, App1
18	1205.5	95.2	280	US-10-880-922-56	Sequence 56, App1
19	1204.5	95.1	280	US-10-880-922-60	Sequence 60, App1
20	1201.5	94.9	280	US-10-880-922-61	Sequence 61, App1
21	1200.5	94.8	280	US-10-880-922-55	Sequence 55, App1
22	1191.5	94.1	239	US-09-880-748-2015	Sequence 2015, App
23	1191.5	94.1	239	US-10-293-418-2015	Sequence 2015, App
24	1187	93.8	309	US-10-052-798-9	Sequence 9, App1
25	1187	93.8	309	US-10-288-917-9	Sequence 9, App1
26	1187	93.8	309	US-10-423-448-9	Sequence 9, App1
27	1178	93.0	244	US-10-322-672-42	Sequence 42, App1
28	1139.5	90.0	239	US-09-880-748-2018	Sequence 2018, App
29	1139.5	90.0	239	US-10-293-418-2018	Sequence 2018, App
30	1133	89.5	244	US-10-322-672-45	Sequence 45, App1
31	1132.5	89.5	239	US-09-880-748-2035	Sequence 2035, App
32	1132.5	89.5	239	US-10-293-418-2035	Sequence 2035, App
33	1131.5	89.4	245	US-10-322-672-43	Sequence 43, App1
34	1131	89.3	252	US-09-880-748-1416	Sequence 1416, App
35	1131	89.3	252	US-10-293-418-1416	Sequence 1416, App
36	1129.5	89.2	243	US-10-935-290-69	Sequence 69, App1
37	1127.5	89.1	243	US-09-880-748-2056	Sequence 2056, App
38	1127.5	89.1	243	US-10-293-418-2056	Sequence 2056, App
39	1126.5	89.0	239	US-09-880-748-2023	Sequence 2023, App
40	1126.5	89.0	239	US-10-293-418-2023	Sequence 2023, App
41	1121	88.5	242	US-10-935-290-130	Sequence 130, App
42	1120	88.5	291	US-10-406-830-6	Sequence 6, App1
43	1119	88.4	240	US-09-880-748-2013	Sequence 2013, App
44	1119	88.4	240	US-10-293-418-2013	Sequence 2013, App
45	1117.5	88.3	247	US-09-880-748-996	Sequence 996, App

ALIGNMENTS

RESULT 1					
US-10-032-037B-204					
; Sequence 204, Application US/10032037B					
; Publication No. US20040001822A1					
; GENERAL INFORMATION:					
; APPLICANT: Bio-Technology General Corp.					
; TITLE OR INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED					
; FILE REFERENCE: 10793/44					
; CURRENT APPLICATION NUMBER: US/10/032,037B					
; CURRENT FILING DATE: 2001-12-31					
; PRIOR APPLICATION NUMBER: 60/258,948					
; PRIOR FILING DATE: 2000-12-29					
; NUMBER OF SEQ ID NOS: 204					
; SOFTWARE: FastSeq for Windows Version 3.0					
; SEQ ID NO 204					
; LENGTH: 266					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-032-037B-204					
Query Match 100.0%; Score 1266; DB 15; Length 266;					
Best Local Similarity 100.0%; Pred. No. 38-83;					
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MAEVLVESGGGVRRPGSLRLESCASGTFPDYIGSWRQAQKGLFWSGINWNGST	60		
DB	21	MAEVLVESGGGVRRPGSLRLESCASGTFPDYIGSWRQAQKGLFWSGINWNGST	80		
QY	61	GYADSVKGRFTISRDNAKNSLYLQNNSLRADPAVYYCAKMRAPVYWGQSTLTYSRGG	120		
DB	81	GYADSVKGRFTISRDNAKNSLYLQNNSLRADPAVYYCAKMRAPVYWGQSTLTYSRGG	140		
QY	121	GGGGGGGGGGSSSLTQDPVAVSVALGQTVRITCGGSLRSYASWTQOKRGAQPVYVYG	180		
DB	141	GGGGGGGGGGSSSLTQDPVAVSVALGQTVRITCGGSLRSYASWTQOKRGAQPVYVYG	200		

QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260

RESULT 2

US-10-029-988B-204
 ; Sequence 204, Application US/10029988B
 ; Publication No. US20040001839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bio-Technology General Corp.
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; FILE REFERENCE: 10793/46
 ; CURRENT APPLICATION NUMBER: US/10/029, 988B
 ; PRIOR FILING DATE: 2001-12-31
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 204
 ; LENGTH: 266
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 US-10-029-988B-204

Query Match 100.0%; Score 1266; DB 15; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3e-83;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSIRLSCAAGFTFDDYGMWVRQAPGKLEWVSGINWNGST 60
 DB 21 MAEVLVESGGGVRRPGSIRLSCAAGFTFDDYGMWVRQAPGKLEWVSGINWNGST 80
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTTLTVSRGGG 120
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTTLTVSRGGG 140
 QY 121 GSGGGSGGGSSSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 180
 DB 141 GSGGGSGGGSSSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 200
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260

RESULT 3

US-10-032-423A-204
 ; Sequence 204, Application US/10032423A
 ; Publication No. US20040002450A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bio-Technology General Corp.
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; FILE REFERENCE: 10793/45
 ; CURRENT APPLICATION NUMBER: US/10/032, 423A
 ; PRIOR FILING DATE: 2001-12-31
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 204
 ; LENGTH: 266
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 US-10-032-423A-204

Query Match 100.0%; Score 1266; DB 15; Length 266;
 Best Local Similarity 100.0%; Pred. No. 3e-83;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSIRLSCAAGFTFDDYGMWVRQAPGKLEWVSGINWNGST 60
 DB 21 MAEVLVESGGGVRRPGSIRLSCAAGFTFDDYGMWVRQAPGKLEWVSGINWNGST 80
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTTLTVSRGGG 120
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTTLTVSRGGG 140
 QY 121 GSGGGSGGGSSSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 180
 DB 141 GSGGGSGGGSSSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 200
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260

RESULT 4

US-10-032-037B-25
 ; Sequence 25, Application US/10032037B
 ; Publication No. US20040001822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bio-Technology General Corp.
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; FILE REFERENCE: 10793/44
 ; CURRENT APPLICATION NUMBER: US/10/032, 037B
 ; PRIOR FILING DATE: 2001-12-31
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 277
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 US-10-032-037B-25

Query Match 100.0%; Score 1266; DB 15; Length 277;
 Best Local Similarity 100.0%; Pred. No. 3.1e-83;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSIRLSCAAGFTFDDYGMWVRQAPGKLEWVSGINWNGST 60
 DB 21 MAEVLVESGGGVRRPGSIRLSCAAGFTFDDYGMWVRQAPGKLEWVSGINWNGST 80
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTTLTVSRGGG 120
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTTLTVSRGGG 140
 QY 121 GSGGGSGGGSSSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 180
 DB 141 GSGGGSGGGSSSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 200
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260

RESULT 5

US-10-029-988B-25
 ; Sequence 25, Application US/10029988B
 ; Publication No. US20040001839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bio-Technology General Corp.
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; FILE REFERENCE: 10793/46
 ; CURRENT APPLICATION NUMBER: US/10/029, 988B
 ; PRIOR FILING DATE: 2001-12-31
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 204

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-988B-25
```

```
Query Match          100.0%; Score 1266; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 60
    |||
DB 21 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 80
    |||
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 120
    |||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 140
    |||
QY 121 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||
DB 141 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||
QY 181 KNNRPGIGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
    |||
DB 201 KNNRPGIGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260
    |||
```

```
RESULT 6
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-423A-25
```

```
Query Match          100.0%; Score 1266; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 60
    |||
DB 21 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 80
    |||
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 120
    |||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 140
    |||
QY 121 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||
DB 141 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||
QY 181 KNNRPGIGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
    |||
DB 201 KNNRPGIGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260
    |||
```

```
RESULT 7
US-10-029-926B-25
; Sequence 25, Application US/10029926B
```

```
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-926B-25
```

```
Query Match          100.0%; Score 1266; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 60
    |||
DB 21 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 80
    |||
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 120
    |||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 140
    |||
QY 121 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||
DB 141 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||
QY 181 KNNRPGIGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
    |||
DB 201 KNNRPGIGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260
    |||
```

```
RESULT 8
US-10-032-037B-203
```

```
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-037B-203
```

```
Query Match          98.1%; Score 1242; DB 15; Length 277;
Best Local Similarity 97.9%; Pred. No. 1.6e-81;
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 60
    |||
DB 21 MAEVLVESGGGAVRRPGSLRLSCAASGFTFDDYGMSSWRQAPGKLEWVSGINWNGST 80
    |||
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 120
    |||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAMRAPVIMGGSTLVTSRGGG 140
    |||
QY 121 GSGGGGSGGGSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||
```

Db 141 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 200
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 240
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 260

RESULT 9
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029, 988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match 98.1%; Score 1242; DB 15; Length 277;
Best Local Similarity 97.9%; Pred. No. 1.6e-81;
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAEVLVESGGGAVVRPGGSLRLSCAASGFTEDDYGMKSWRQAPGKLEWVSGINMNGST 60
Db 21 MAEVLVESGGGAVVRPGGSLRLSCAASGFTEDDYGMKSWRQAPGKLEWVSGINMNGST 80
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAARMAPVIMGGSTLTVSRGG 120
Db 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAARMAPVIMGGSTLTVSRGG 140
QY 121 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 180
Db 141 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 200
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 240
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 260

RESULT 10
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032, 423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 98.1%; Score 1242; DB 15; Length 277;
Best Local Similarity 97.9%; Pred. No. 1.6e-81;
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGAVVRPGGSLRLSCAASGFTEDDYGMKSWRQAPGKLEWVSGINMNGST 60
Db 21 MAEVLVESGGGAVVRPGGSLRLSCAASGFTEDDYGMKSWRQAPGKLEWVSGINMNGST 80
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAARMAPVIMGGSTLTVSRGG 120
Db 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAARMAPVIMGGSTLTVSRGG 140
QY 121 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 180
Db 141 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 200
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 240
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 260

RESULT 11
US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040007301A1
; GENERAL INFORMATION:
; APPLICANT: HUGAT, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029, 926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-203

Query Match 98.1%; Score 1242; DB 15; Length 277;
Best Local Similarity 97.9%; Pred. No. 1.6e-81;
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAEVLVESGGGAVVRPGGSLRLSCAASGFTEDDYGMKSWRQAPGKLEWVSGINMNGST 60
Db 21 MAEVLVESGGGAVVRPGGSLRLSCAASGFTEDDYGMKSWRQAPGKLEWVSGINMNGST 80
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAARMAPVIMGGSTLTVSRGG 120
Db 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAARMAPVIMGGSTLTVSRGG 140
QY 121 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 180
Db 141 GSGGGGGGGGGSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYG 200
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 240
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYCNRSRDSGNHVVFGGKTLTVLG 260

RESULT 12
US-09-880-748-937
; Sequence 937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880, 748
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17

;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 937
;; LENGTH: 239
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-880-748-937

Query Match 96.2%; Score 1218.5; DB 10; Length 239;
Best Local Similarity 97.9%; Pred. No. 6.9e-80;

Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVAPGSGSLRLSCAASGFTFDYGMGHWVQAPEGKLEWVSGINMGSGTGY 62
|||
DB 1 EVOLVESGGGVAPGSGSLRLSCAASGFTFDYGMGHWVQAPEGKLEWVSGINMGSGTGY 60
|||
QY 63 ADSVKGRFTISRDNKAKSLYLQNMSLRAEDTAVYYCARMR-APVIMQGTLVTVSRGGG 121
|||
DB 61 ADSVKGRFTISRDNKAKSLYLQNMSLRAEDTAVYYCARRRYALDYWGQGLVTVSRGGG 120
|||
QY 122 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLYYK 181
|||
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLYYK 180
|||
QY 182 NNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVPFGGTLVYLG 240
|||
DB 181 NNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVPFGGTLVYLG 239
|||

RESULT 13
US-10-293-418-937
;; Sequence 937, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruden et al.
;; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
;; FILE REFERENCE: PFS23P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 937
;; LENGTH: 239
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-10-293-418-937

Query Match 96.2%; Score 1218.5; DB 15; Length 239;
Best Local Similarity 97.9%; Pred. No. 6.9e-80;

Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVAPGSGSLRLSCAASGFTFDYGMGHWVQAPEGKLEWVSGINMGSGTGY 62

DB 1 EVOLVESGGGVAPGSGSLRLSCAASGFTFDYGMGHWVQAPEGKLEWVSGINMGSGTGY 60
|||
QY 63 ADSVKGRFTISRDNKAKSLYLQNMSLRAEDTAVYYCARMR-APVIMQGTLVTVSRGGG 121
|||
DB 61 ADSVKGRFTISRDNKAKSLYLQNMSLRAEDTAVYYCARRRYALDYWGQGLVTVSRGGG 120
|||
QY 122 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLYYK 181
|||
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLYYK 180
|||
QY 182 NNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVPFGGTLVYLG 240
|||
DB 181 NNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVPFGGTLVYLG 239
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RESULT 14
US-10-880-922-6
;; Sequence 6, Application US/10880922
;; Publication No. US2005006955A1
;; GENERAL INFORMATION:
;; APPLICANT: PLAKSIN, DANIEL
;; APPLICANT: LEVANNON, AVIGDOR
;; APPLICANT: SZANTON, ESTHER
;; APPLICANT: HAGAY, YOCHVED
;; APPLICANT: BEN-LEVY, RACHEL
;; APPLICANT: NISGAV, YAEI
;; APPLICANT: KANFT, YARIV
;; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
;; FILE REFERENCE: 10793-143
;; CURRENT APPLICATION NUMBER: US/10/880,922
;; CURRENT FILING DATE: 2004-06-30
;; PRIOR APPLICATION NUMBER: 60/484,061
;; PRIOR FILING DATE: 2003-06-30
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 6
;; LENGTH: 280
;; TYPE: PR1
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: consensus antibody
US-10-880-922-6

Query Match 95.9%; Score 1214.5; DB 17; Length 280;
Best Local Similarity 96.3%; Pred. No. 1.6e-79;

Matches 234; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MAEVLVESGGGVAPRGGSLRLSCAASGFTFDYGMGHWVQAPEGKLEWVSGINMG 57
|||
DB 21 MAEVLVESGGGVAPRGGSLRLSCAASGFTFDYGMGHWVQAPEGKLEWVSGINMG 80
|||
QY 58 GSTGVADSVKGRFTISRDNKAKSLYLQNMSLRAEDTAVYYCARMR-APVIMQGTLVTVSR 117
|||
DB 81 GSTGVADSVKGRFTISRDNKAKSLYLQNMSLRAEDTAVYYCARMR-APVIMQGTLVTVSR 140
|||
QY 118 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLY 177
|||
DB 141 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLY 200
|||
QY 178 IYKNNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVPFGGTLT 237
|||
DB 201 IYKNNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVPFGGTLT 260
|||
QY 238 VLG 240
|||
DB 261 VLG 263
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RESULT 15
US-09-880-748-2038
;; Sequence 2038, Application US/09880748

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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2038

Query Match          95.8%; Score 1212.5; DB 10; Length 239;
Best Local Similarity 97.5%; Pred. No. 1.9e-79;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      3  EVLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTVRQAPGKGLEWVSGINNNGSGSTGY 62
        1  EVLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTVRQAPGKGLEWVSGINNNGSGSTGY 60
Db
QY      63  ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAHR-APVWGQGLTVTSRGGGG 121
        61  ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARRRYALDYWGQGLTVTSRGGGG 120
Db
QY      122  SGGGSGGGSSSELTQDPAYVALGQTVRIITCGDSLRSYYASWYQKPGQAPVLYYGR 181
        121  SGGGSGGGSSSELTQDPAYVALGQTVRIITCGDSLRSYYASWYQKPGQAPVLYYGR 180
Db
QY      182  NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTYLTVLG 240
        181  NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTYLTVLG 239
Db
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Search completed: April 25, 2005, 21:09:50
Job time : 107.164 secs